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(54) Title: NOVEL MAMMALIAN G-PROTEIN COUPLED RECEPTORS HAVING EXTRACELLULAR LEUCINE RICH REPEAT REGIONS (57) Abstract Isolated nucleotide compositions and sequences are provided for LGR4, LGR5 and LGR7 genes. The nucleic acid compositions find use in identifying homologous or related genes; in identifying endogenous ligands for these receptors; in producing compositions that modulate the expression or function of its encoded protein; for gene therapy; mapping functional regions of the protein; and in studying associated physiological pathways. In addition, modulation of the gene activity <i>in vivo</i> is used for prophylactic and therapeutic purposes.		

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NOVEL MAMMALIAN G-PROTEIN COUPLED RECEPTORS HAVING EXTRACELLULAR LEUCINE RICH REPEAT REGIONS

INTRODUCTION

5 Field of the Invention

The field of this invention is the G-protein coupled receptor family of proteins.

Background

Gonadotropins (Luteinizing hormone, LH; follicle stimulating hormone, FSH; chorionic gonadotropin, CG) and thyrotropin (TSH)) are essential for the growth and
10 differentiation of gonads and thyroid gland, respectively. These glycoprotein hormones bind specific target cell receptors on the plasma membrane to activate the cAMP-protein kinase A pathway.

The receptors for LH, FSH and TSH belong to the large G-protein-coupled, seven-trans-membrane protein family but are unique in having a large N-terminal extra-cellular
15 (ecto-) domain containing leucine-rich repeats important for interaction with large glycoprotein ligands. Studies suggest that in these receptors, the extra-cellular leucine rich repeat region serves as a "baseball glove" which efficiently catches its corresponding large hormone ligand and optimally orients it for interaction with the seven trans-membrane-helical domain of the receptor.

20 Because hormones and receptors play a prominent role in a variety of physiological processes, there is continued interest in the identification of novel receptors and their ligands, as well as the genes encoding the same.

Relevant Literature

References of interest include: el Tayar, N, "Advances in the Molecular
25 Understanding of Gonadotropins-Receptors Interactions," Mol. Cell. Endocrinol. (December 20, 1996) 125: 65-70; Bhowmick et al., "Determination of Residues Important in Hormone Binding to the Extracellular Domain of the Luteinizing Hormone/Chorionic Gonadotropin Receptor by Site-Directed Mutagenesis and Modeling," Mol. Endocrinol. (September 1996) 10: 1147-1159; Thomas et al., "Mutational Analyses of the
30 Extracellular Domain of the Full-Length Lutropin/Choriogonadotropin Receptor Suggest Leucine-Rich Repeats 1-6 are Involved in Hormone Binding," Mol. Endocrinol. (June 1996) 10:760-768; Segaloff & Ascoli, "The Gonadotropin Receptors: Insights from the

Cloning of their cDNAs," Oxf. Rev. Reprod. Biol. (1992) 14: 141-168; Braun et al., "Amino-Terminal Leucine-Rich Repeats in Gonadotropin Receptors Determine Hormone Selectivity," EMBO J (July 1991) 10: 1885-1890; and Segaloff et al., "Structure of the Lutropin/Choriogonadotropin Receptor," Recent Prog. Horm. Res. (1990) 46: 261-301.

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SUMMARY OF THE INVENTION

Three novel mammalian G-protein coupled receptors having extra-cellular leucine rich repeat domains, i.e. LGR4, LGR5 and LGR7, and polypeptide compositions related thereto, as well as nucleotide compositions encoding the same, are provided. The subject
10 proteins, polypeptide and nucleic acid compositions find use in a variety of different applications, including the identification of homologous or related genes; the production of compositions that modulate the expression or function of the subject proteins; in the identification of endogenous ligands for the subject orphan receptors; in the generation of functional binding proteins for the neutralization of the actions of endogenous ligands; in
15 gene therapy; in mapping functional regions of the protein; and in studying associated physiological pathways. In addition, modulation of the gene activity *in vivo* is used for prophylactic and therapeutic purposes, and the like.

BRIEF DESCRIPTION OF THE FIGURES

- 20 Fig. 1 provides the nucleotide and amino acid sequence for human LGR4.
Fig. 2 provides the nucleotide and amino acid sequence for human LGR5.
Fig. 3 provides the nucleotide and amino acid sequence for human LGR7, long form.
Fig. 4 provides the nucleotide and amino acid sequence for human LGR7, short
25 form.
Fig. 5 provides an alignment comparison of the long and short forms of LGR7.
Figs. 6 provides a comparison of deduced amino acid sequence of LGR4 and 5 cDNAs and those encoding FSH and LH receptors.

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DESCRIPTION OF THE SPECIFIC EMBODIMENTS

Novel mammalian G-protein coupled receptors having extra-cellular leucine rich repeat regions (i.e. LGR4, LGR5 and LGR7) and polypeptide compositions related thereto, as well as nucleic acid compositions encoding the same, are provided. The
5 subject polypeptide and/or nucleic acid compositions find use in a variety of different applications, including the identification of homologous or related genes; for the identification of endogenous ligands for these novel receptors; the production of compositions that modulate the expression or function of the receptors; for gene therapy; for mapping functional regions of the receptors; in studying associated physiological
10 pathways; for *in vivo* prophylactic and therapeutic purposes; as immunogens for producing antibodies; in screening for biologically active agents; and the like.

Before the subject invention is further described, it is to be understood that the invention is not limited to the particular embodiments of the invention described below, as
15 variations of the particular embodiments may be made and still fall within the scope of the appended claims. It is also to be understood that the terminology employed is for the purpose of describing particular embodiments, and is not intended to be limiting. Instead, the scope of the present invention will be established by the appended claims.

20 In this specification and the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

25 CHARACTERIZATION OF LGR4, LGR5 AND LGR7

LGR4, LGR5 and LGR7 are novel mammalian receptors of the G-protein coupled, seven trans-membrane family of proteins, specifically the subfamily of G-protein coupled seven trans-membrane proteins which are characterized by the presence of extra-cellular leucine rich repeat regions. As such, these proteins have trans-membrane segments and
30 extra-cellular regions similar to those found in the known LH, FSH, and TSH receptors. In other words, these proteins have both a G-protein coupled seven trans-membrane region

and a leucine rich repeat extra-cellular domain. The N-terminal extra-cellular domains of these proteins also show high homology with *Drosophila* Slit and Toll proteins having leucine rich repeats. These proteins are expressed in diverse tissues.

The human LGR4 gene has a nucleotide sequence as shown in SEQ ID NO:01.

5 The human LGR4 gene product has an amino acid sequence as shown in SEQ ID NO:02. LGR4 is expressed in a plurality of different tissue types, including ovary, testis, adrenal, placenta, liver, kidney and intestine.

The human LGR5 gene has a nucleotide sequence as shown in SEQ ID NO:03.

The LGR5 gene product has an amino acid sequence as shown in SEQ ID NO:04. LGR5
10 has been found to be mainly expressed in muscle, placenta and spinal cord tissue.

The human LGR7 gene encodes multiple splicing variants, each of which contains a multitude of cysteine-rich low density lipoprotein (LDL) binding motifs at the N-terminus in addition to the leucine rich repeat region. The longer forms of LGR-7 have a higher similarity than shorter forms of LGR-7 to snail LGR in the trans-membrane domain
15 and the N-terminal LDL binding domain. The overall structure of both the long and short forms of LGR-7 is similar to that of the LH receptor. The human LGR7 short form gene has a nucleotide sequence as shown in SEQ ID NO:05. The LGR7 short form gene product has an amino acid sequence as shown in SEQ ID NO:06. The human LGR7 long form gene has a nucleotide sequence as shown in SEQ ID NO:07. The LGR7 long form
20 gene product has an amino acid sequence as shown in SEQ ID NO:08. LGR7 is expressed in multiple tissues, including testis, ovary, prostate, intestine and colon.

IDENTIFICATION OF *LGR4*, *LGR5* AND *LGR7* SEQUENCES

Homologs of *LGR4*, *LGR5* and *LGR7* are identified by any of a number of
25 methods. A fragment of the provided cDNA may be used as a hybridization probe against a cDNA library from the target organism of interest, where low stringency conditions are used. The probe may be a large fragment, or one or more short degenerate primers.

Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 6×SSC (0.9 M sodium chloride/0.09 M
30 sodium citrate) and remain bound when subjected to washing at 55°C in 1×SSC (0.15 M sodium chloride/0.015 M sodium citrate). Sequence identity may be determined by

hybridization under stringent conditions, for example, at 50°C or higher and 0.1×SSC (15 mM sodium chloride/0.15 mM sodium citrate). Nucleic acids having a region of substantial identity to the provided *LGR4*, *LGR5* and/or *LGR7* sequences, e.g. allelic variants, genetically altered versions of the gene, etc., bind to the provided sequences under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous genes may be any species, e.g., primate species, particularly human; rodents, such as rats and mice; canines; felines; bovines; ovines; equines; yeast; nematodes; etc.

Between mammalian species, e.g., human and mouse, homologs have substantial sequence similarity, e.g. at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, etc. A reference sequence will usually be at least about 18 nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul *et al.* (1990), *J. Mol. Biol.* **215**:403-10. Unless specified otherwise, all sequence analysis numbers provided herein are as determined with the BLAST program using default settings. The sequences provided herein are essential for recognizing *LGR4*, *LGR5* and *LGR7*-related and homologous proteins in database searches.

LGR4, *LGR5* and *LGR7* NUCLEIC ACID COMPOSITIONS

Nucleic acids encoding *LGR4*, *LGR5* and *LGR7* may be cDNA or genomic DNA or a fragment thereof. The terms "*LGR4* gene," "*LGR5* gene" and "*LGR7* gene" shall be intended to mean the open reading frame encoding specific *LGR4*, *LGR5* and *LGR7* polypeptides, and *LGR4*, *LGR5* and *LGR7* introns, as well as adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but possibly further in either direction. The gene may be introduced into an appropriate vector for extra-chromosomal maintenance or for integration into a host genome.

The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, removed by nuclear
5 RNA splicing, to create a continuous open reading frame encoding an LGR4, LGR5 and LGR7 protein.

A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It may further include the 3'
10 and 5' untranslated regions found in the mature mRNA. It may further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' or 3' end of the transcribed region. The genomic DNA may be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic
15 DNA flanking the coding region, either 3' or 5', or internal regulatory sequences as sometimes found in introns, contains sequences required for proper tissue and stage specific expression.

The sequence of the 5' flanking region may be utilized for promoter elements, including enhancer binding sites, that provide for developmental regulation in tissues
20 where *LGR4*, *LGR5* and/or *LGR7* is expressed. The tissue specific expression is useful for determining the pattern of expression, and for providing promoters that mimic the native pattern of expression. Naturally occurring polymorphisms in the promoter region are useful for determining natural variations in expression, particularly those that may be associated with disease.

Alternatively, mutations may be introduced into the promoter region to determine
25 the effect of altering expression in experimentally defined systems. Methods for the identification of specific DNA motifs involved in the binding of transcriptional factors are known in the art, *e.g.* sequence similarity to known binding motifs, gel retardation studies, *etc.* For examples, see Blackwell *et al.* (1995), *Mol. Med.* 1:194-205; Mortlock *et al.*
30 (1996), *Genome Res.* 6:327-33; and Joulin and Richard-Foy (1995), *Eur. J. Biochem.* 232:620-626.

The regulatory sequences may be used to identify *cis* acting sequences required for transcriptional or translational regulation of *LGR4*, *LGR5* and/or *LGR7* expression, especially in different tissues or stages of development, and to identify *cis* acting sequences and *trans*-acting factors that regulate or mediate *LGR4*, *LGR* and/or *LGR7* expression. Such transcription or translational control regions may be operably linked to an *LGR4*, *LGR5* or *LGR7* gene in order to promote expression of wild type or altered *LGR4*, *LGR5* or *LGR7* or other proteins of interest in cultured cells, or in embryonic, fetal or adult tissues, and for gene therapy.

The nucleic acid compositions of the subject invention may encode all or a part of the subject polypeptides. Double or single stranded fragments may be obtained of the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.* For the most part, DNA fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and may be at least about 50 nt. Such small DNA fragments are useful as primers for PCR, hybridization screening probes, *etc.* Larger DNA fragments, *i.e.* greater than 100 nt are useful for production of the encoded polypeptide. For use in amplification reactions, such as PCR, a pair of primers will be used. The exact composition of the primer sequences is not critical to the invention, but for most applications the primers will hybridize to the subject sequence under stringent conditions, as known in the art. It is preferable to choose a pair of primers that will generate an amplification product of at least about 50 nt, preferably at least about 100 nt. Algorithms for the selection of primer sequences are generally known, and are available in commercial software packages. Amplification primers hybridize to complementary strands of DNA, and will prime towards each other.

The *LGR4*, *LGR* and *LGR7* genes are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the DNA will be obtained substantially free of other nucleic acid sequences that do not include an *LGR4*, *LGR5* or *LGR7* sequence or fragment thereof, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant", *i.e.* flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

The DNA may also be used to identify expression of the gene in a biological specimen. The manner in which one probes cells for the presence of particular nucleotide

sequences, as genomic DNA or RNA, is well established in the literature and does not require elaboration here. DNA or mRNA is isolated from a cell sample. The mRNA may be amplified by RT-PCR, using reverse transcriptase to form a complementary DNA strand, followed by polymerase chain reaction amplification using primers specific for the
5 subject DNA sequences. Alternatively, the mRNA sample is separated by gel electrophoresis, transferred to a suitable support, *e.g.* nitrocellulose, nylon, *etc.*, and then probed with a fragment of the subject DNA as a probe. Other techniques, such as oligonucleotide ligation assays, *in situ* hybridizations, and hybridization to DNA probes arrayed on a solid chip may also find use. Detection of mRNA hybridizing to the subject
10 sequence is indicative of *LGR4*, *LGR5* and/or *LGR7* gene expression in the sample.

The sequence of an *LGR4*, *LGR5* or *LGR7* gene, including flanking promoter regions and coding regions, may be mutated in various ways known in the art to generate targeted changes in promoter strength, sequence of the encoded protein, *etc.* The DNA sequence or protein product of such a mutation will usually be substantially similar to the
15 sequences provided herein, *i.e.* will differ by at least one nucleotide or amino acid, respectively, and may differ by at least two but not more than about ten nucleotides or amino acids. The sequence changes may be substitutions, insertions, deletions, or a combination thereof. Deletions may further include larger changes, such as deletions of a domain or exon. Other modifications of interest include epitope tagging, *e.g.* with the
20 FLAG system, HA, *etc.* For studies of subcellular localization, fusion proteins with green fluorescent proteins (GFP) may be used.

Techniques for *in vitro* mutagenesis of cloned genes are known. Examples of protocols for site specific mutagenesis may be found in Gustin *et al.* (1993), *Biotechniques* 14:22; Barany (1985), *Gene* 37:111-23; Colicelli *et al.* (1985), *Mol. Gen.*
25 *Genet.* 199:537-9; and Prentki *et al.* (1984), *Gene* 29:303-13. Methods for site specific mutagenesis can be found in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, CSH Press 1989, pp. 15.3-15.108; Weiner *et al.* (1993), *Gene* 126:35-41; Sayers *et al.* (1992), *Biotechniques* 13:592-6; Jones and Winistorfer (1992), *Biotechniques* 12:528-30; Barton *et al.* (1990), *Nucleic Acids Res* 18:7349-55; Marotti and Tomich (1989), *Gene*
30 *Anal. Tech.* 6:67-70; and Zhu (1989), *Anal Biochem* 177:120-4. Such mutated genes may

be used to study structure-function relationships of LGR4, LGR5 and/or LGR7, or to alter properties of the protein that affect its function or regulation.

LGR4, LGR5 and LGR7 POLYPEPTIDES

5 Also provided by the subject invention are LGR4, LGR5 and LGR7 polypeptide compositions. The term polypeptide composition as used herein refers to both the full length proteins as well as portions or fragments thereof. Also included in this term are variations of the naturally occurring proteins, where such variations are homologous or substantially similar to the naturally occurring protein, be the naturally occurring protein
10 the human protein, mouse protein, or protein from some other species which naturally expresses an LGR4, LGR5 or LGR7 protein, usually a mammalian species. A candidate homologous protein is substantially similar to an LGR4, LGR5 or LGR7 protein of the subject invention, and therefore is an LGR4, LGR5 or LGR7 protein of the subject invention, if the candidate protein has a sequence that has at least about 80%, usually at
15 least about 90% and more usually at least about 98% sequence identity with an LGR4, LGR5 or LGR7 protein, as measured by BLAST, supra. In the following description of the subject invention, the term "LGR4, LGR5 or LGR7-protein" is used to refer not only to the human LGR4, LGR5 or LGR7 protein, but also to homologs thereof expressed in non-human species, e.g. murine, rat and other mammalian species.

20 The subject gene may be employed for producing all or portions of LGR4, LGR5 and LGR7 polypeptides. By "LGR4 polypeptide/protein", "LGR5 polypeptide/protein," and "LGR7 polypeptide/protein" is meant an amino acid sequence encoded by an open reading frame (ORF) of *LGR4*, *LGR5* and *LGR7* genes, including the full-length native polypeptide and fragments thereof, particularly biologically active fragments and/or
25 fragments corresponding to functional domains, e.g. extra-cellular regions; and including fusions of the subject polypeptides to other proteins or parts thereof, e.g. chimeric proteins. For expression, an expression cassette may be employed. The expression vector will provide a transcriptional and translational initiation region, which may be inducible or constitutive, where the coding region is operably linked under the transcriptional control
30 of the transcriptional initiation region, and a transcriptional and translational termination

region. These control regions may be native to an *LGR4*, *LGR5* or *LGR7* gene, or may be derived from exogenous sources.

Expression vectors generally have convenient restriction sites located near the promoter sequence to provide for the insertion of nucleic acid sequences encoding
5 heterologous proteins. A selectable marker operative in the expression host may be present. Expression vectors may be used for the production of fusion proteins, where the exogenous fusion peptide provides additional functionality, i.e. increased protein synthesis, stability, reactivity with defined antisera, an enzyme marker, e.g. β -galactosidase, etc.

10 Expression cassettes may be prepared comprising a transcription initiation region, the gene or fragment thereof, and a transcriptional termination region. Of particular interest is the use of sequences that allow for the expression of functional epitopes or domains, usually at least about 8 amino acids in length, more usually at least about 15 amino acids in length, to about 25 amino acids, and up to the complete open reading frame
15 of the gene. After introduction of the DNA, the cells containing the construct may be selected by means of a selectable marker, the cells expanded and then used for expression.

LGR4, LGR5 or LGR7 polypeptides may be expressed in prokaryotes or eukaryotes in accordance with conventional ways, depending upon the purpose for expression. For large scale production of the protein, a unicellular organism, such as *E. coli*, *B. subtilis*, *S. cerevisiae*, insect cells in combination with baculovirus vectors, or cells
20 of a higher organism such as vertebrates, particularly mammals, e.g. COS 7 cells, may be used as the expression host cells. In some situations, it is desirable to express the *LGR4*, *LGR5* or *LGR7* gene in eukaryotic cells, where the LGR4, LGR5 or LGR7 protein will benefit from native folding and post-translational modifications. Small peptides can also
25 be synthesized in the laboratory. Polypeptides that are subsets of the complete LGR4, LGR5 or LGR7 sequence may be used to identify and investigate parts of the protein important for function or to raise antibodies directed against these regions.

For production of the extracellular domain of the LGR4, LGR5 or LGR7 receptor, the anchored receptor approach as described in Osuga et al, Mol. Endocrinol. (1997) 11:
30 1659-1668 may be employed. Likewise, the chimeric receptor approach described in Kudo et al, J Biol. Chem. (1996) 271; 22470-22478 may be used.

Such peptides find use in the identification of endogenous ligands and in drug screening for agonists and antagonists using methods described in Osuga, supra. Solubilized extracellular domains find use as therapeutic agents, e.g. in the neutralization of the action of endogenous ligands.

5 With the availability of the protein or fragments thereof in large amounts, by employing an expression host, the protein may be isolated and purified in accordance with conventional ways. A lysate may be prepared of the expression host and the lysate purified using HPLC, exclusion chromatography, gel electrophoresis, affinity chromatography, or other purification technique. The purified protein will generally be at
10 least about 80% pure, preferably at least about 90% pure, and may be up to and including 100% pure. Pure is intended to mean free of other proteins, as well as cellular debris.

 The expressed LGR4, LGR5 and LGR7 polypeptides are useful for the production of antibodies, where short fragments provide for antibodies specific for the particular polypeptide, and larger fragments or the entire protein allow for the production of
15 antibodies over the surface of the polypeptide. Antibodies may be raised to the wild-type or variant forms of LGR4, LGR5 or LGR7. Antibodies may be raised to isolated peptides corresponding to these domains, or to the native protein.

 Antibodies are prepared in accordance with conventional ways, where the expressed polypeptide or protein is used as an immunogen, by itself or conjugated to
20 known immunogenic carriers, e.g. KLH, pre-S HBsAg, other viral or eukaryotic proteins, or the like. Various adjuvants may be employed, with a series of injections, as appropriate. Both polyclonal and monoclonal antibodies may be produced. For monoclonal antibodies, after one or more booster injections, the spleen is isolated, the lymphocytes immortalized by cell fusion, and then screened for high affinity antibody
25 binding. The immortalized cells, i.e. hybridomas, producing the desired antibodies may then be expanded. For further description, see Monoclonal Antibodies: A Laboratory Manual, Harlow and Lane eds., Cold Spring Harbor Laboratories, Cold Spring Harbor, New York, 1988. If desired, the mRNA encoding the heavy and light chains may be isolated and mutagenized by cloning in *E. coli*, and the heavy and light chains mixed to
30 further enhance the affinity of the antibody. Alternatives to *in vivo* immunization as a

method of raising antibodies include binding to phage "display" libraries, usually in conjunction with *in vitro* affinity maturation.

DIAGNOSTIC USES

5 The subject nucleic acid and/or polypeptide compositions may be used to analyze a patient sample for the presence of polymorphisms associated with a disease state or genetic predisposition to a disease state. Biochemical studies may be performed to determine whether a sequence polymorphism in an *LGR4*, *LGR* or *LGR7* coding region or control regions is associated with disease. Disease associated polymorphisms may include
10 deletion or truncation of the gene, mutations that alter expression level, that affect the activity of the protein, and the like.

Changes in the promoter or enhancer sequence that may affect expression levels of *LGR4*, *LGR5* or *LGR7* can be compared to expression levels of the normal allele by various methods known in the art. Methods for determining promoter or enhancer
15 strength include quantitation of the expressed natural protein; insertion of the variant control element into a vector with a reporter gene such as β -galactosidase, luciferase, chloramphenicol acetyltransferase, *etc.*, that provides for convenient quantitation; and the like.

A number of methods are available for analyzing nucleic acids for the presence of
20 a specific sequence, *e.g.* a disease associated polymorphism. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. Cells that express *LGR4*, *LGR5* or *LGR7* may be used as a source of mRNA, which may be assayed directly or reverse transcribed into cDNA for analysis. The nucleic acid may be amplified
25 by conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis. The use of the polymerase chain reaction is described in Saiki, *et al.* (1985), *Science* 239:487, and a review of techniques may be found in Sambrook, *et al.* Molecular Cloning: A Laboratory Manual, CSH Press 1989, pp.14.2–14.33. Alternatively, various methods are known in the art that utilize oligonucleotide
30 ligation as a means of detecting polymorphisms, for examples see Riley *et al.* (1990),

Nucl. Acids Res. 18:2887-2890; and Delahunty *et al.* (1996), *Am. J. Hum. Genet.* 58:1239-1246.

A detectable label may be included in an amplification reaction. Suitable labels include fluorochromes, *e.g.* fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein (JOE), 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA), radioactive labels, *e.g.* ^{32}P , ^{35}S , ^3H ; *etc.* The label may be a two stage system, where the amplified DNA is conjugated to biotin, haptens, *etc.* having a high affinity binding partner, *e.g.* avidin, specific antibodies, *etc.*, where the binding partner is conjugated to a detectable label. The label may be conjugated to one or both of the primers. Alternatively, the pool of nucleotides used in the amplification is labeled, so as to incorporate the label into the amplification product.

The sample nucleic acid, *e.g.* amplified or cloned fragment, is analyzed by one of a number of methods known in the art. The nucleic acid may be sequenced by dideoxy or other methods, and the sequence of bases compared to a wild-type *LGR4*, *LGR5* or *LGR7* sequence. Hybridization with the variant sequence may also be used to determine its presence, by Southern blots, dot blots, *etc.* The hybridization pattern of a control and variant sequence to an array of oligonucleotide probes immobilized on a solid support, as described in US 5,445,934, or in WO 95/35505 (the disclosures of which are herein incorporated by reference), may also be used as a means of detecting the presence of variant sequences. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility. Alternatively, where a polymorphism creates or destroys a recognition site for a restriction endonuclease, the sample is digested with that endonuclease, and the products size fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

Screening for mutations in *LGR4*, *LGR5* or *LGR7* may be based on the functional or antigenic characteristics of the protein. Protein truncation assays are useful in detecting

deletions that may affect the biological activity of the protein. Various immunoassays designed to detect polymorphisms in LGR4, LGR5 or LGR7 proteins may be used in screening. Where many diverse genetic mutations lead to a particular disease phenotype, functional protein assays have proven to be effective screening tools. The activity of the encoded LGR4, LGR5 or LGR7 protein may be determined by comparison with the wild-type protein.

Antibodies specific for LGR4, LGR5 or LGR7 proteins may be used in staining or in immunoassays. Samples, as used herein, include biological fluids such as semen, blood, cerebrospinal fluid, tears, saliva, lymph, dialysis fluid and the like; organ or tissue culture derived fluids; and fluids extracted from physiological tissues. Also included in the term are derivatives and fractions of such fluids. The cells may be dissociated, in the case of solid tissues, or tissue sections may be analyzed. Alternatively a lysate of the cells may be prepared.

Diagnosis may be performed by a number of methods to determine the absence or presence or altered amounts of normal or abnormal LGR4, LGR5 or LGR7 in patient cells. For example, detection may utilize staining of cells or histological sections, performed in accordance with conventional methods. Cells are permeabilized to stain cytoplasmic molecules. The antibodies of interest are added to the cell sample, and incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody may be labeled with radioisotopes, enzymes, fluorescers, chemiluminescers, or other labels for direct detection. Alternatively, a second stage antibody or reagent is used to amplify the signal. Such reagents are well known in the art. For example, the primary antibody may be conjugated to biotin, with horseradish peroxidase-conjugated avidin added as a second stage reagent. Alternatively, the secondary antibody conjugated to a fluorescent compound, *e.g.* fluorescein, rhodamine, Texas red, *etc.* Final detection uses a substrate that undergoes a color change in the presence of the peroxidase. The absence or presence of antibody binding may be determined by various methods, including flow cytometry of dissociated cells, microscopy, radiography, scintillation counting, *etc.*

Diagnostic screening may also be performed for polymorphisms that are genetically linked to a disease predisposition, particularly through the use of microsatellite

markers or single nucleotide polymorphisms. Frequently the microsatellite polymorphism itself is not phenotypically expressed, but is linked to sequences that result in a disease predisposition. However, in some cases the microsatellite sequence itself may affect gene expression. Microsatellite linkage analysis may be performed alone, or in combination
5 with direct detection of polymorphisms, as described above. The use of microsatellite markers for genotyping is well documented. For examples, see Mansfield *et al.* (1994), *Genomics* 24:225-233; Ziegle *et al.* (1992), *Genomics* 14:1026-1031; Dib *et al.*, *supra*.

MODULATION OF *LGR4*, *LGR5* and *LGR7* GENE EXPRESSION

10 The *LGR4*, *LGR5* or *LGR7* genes, gene fragments, or the *LGR4*, *LGR5* or *LGR7* protein or protein fragments, are useful in gene therapy to treat disorders associated with *LGR4*, *LGR5* or *LGR7* defects. Expression vectors may be used to introduce the *LGR4*, *LGR5* or *LGR7* gene into a cell. Such vectors generally have convenient restriction sites located near the promoter sequence to provide for the insertion of nucleic acid sequences.
15 Transcription cassettes may be prepared comprising a transcription initiation region, the target gene or fragment thereof, and a transcriptional termination region. The transcription cassettes may be introduced into a variety of vectors, *e.g.* plasmid; retrovirus, *e.g.* lentivirus; adenovirus; and the like, where the vectors are able to transiently or stably be maintained in the cells, usually for a period of at least about one day, more usually for a
20 period of at least about several days to several weeks.

The gene or *LGR4*, *LGR5* or *LGR7* protein may be introduced into tissues or host cells by any number of routes, including viral infection, microinjection, or fusion of vesicles. Jet injection may also be used for intramuscular administration, as described by Furth *et al.* (1992), *Anal Biochem* 205:365-368. The DNA may be coated onto gold
25 microparticles, and delivered intradermally by a particle bombardment device, or "gene gun" as described in the literature (see, for example, Tang *et al.* (1992), *Nature* 356:152-154), where gold microprojectiles are coated with the *LGR4*, *LGR5* or *LGR7* DNA, then bombarded into skin cells.

Antisense molecules can be used to down-regulate expression of *LGR4*, *LGR5*, or
30 *LGR7* in cells. The anti-sense reagent may be antisense oligonucleotides (ODN), particularly synthetic ODN having chemical modifications from native nucleic acids, or

nucleic acid constructs that express such anti-sense molecules as RNA. The antisense sequence is complementary to the mRNA of the targeted gene, and inhibits expression of the targeted gene products. Antisense molecules inhibit gene expression through various mechanisms, *e.g.* by reducing the amount of mRNA available for translation, through
5 activation of RNase H, or steric hindrance. One or a combination of antisense molecules may be administered, where a combination may comprise multiple different sequences.

Antisense molecules may be produced by expression of all or a part of the target gene sequence in an appropriate vector, where the transcriptional initiation is oriented such that an antisense strand is produced as an RNA molecule. Alternatively, the
10 antisense molecule is a synthetic oligonucleotide. Antisense oligonucleotides will generally be at least about 7, usually at least about 12, more usually at least about 20 nucleotides in length, and not more than about 500, usually not more than about 50, more usually not more than about 35 nucleotides in length, where the length is governed by efficiency of inhibition, specificity, including absence of cross-reactivity, and the like. It
15 has been found that short oligonucleotides, of from 7 to 8 bases in length, can be strong and selective inhibitors of gene expression (see Wagner *et al.* (1996), *Nature Biotechnol.* 14:840-844).

A specific region or regions of the endogenous sense strand mRNA sequence is chosen to be complemented by the antisense sequence. Selection of a specific sequence
20 for the oligonucleotide may use an empirical method, where several candidate sequences are assayed for inhibition of expression of the target gene in an *in vitro* or animal model. A combination of sequences may also be used, where several regions of the mRNA sequence are selected for antisense complementation.

Antisense oligonucleotides may be chemically synthesized by methods known in
25 the art (see Wagner *et al.* (1993), *supra*, and Milligan *et al.*, *supra*.) Preferred oligonucleotides are chemically modified from the native phosphodiester structure, in order to increase their intracellular stability and binding affinity. A number of such modifications have been described in the literature, which alter the chemistry of the backbone, sugars or heterocyclic bases.

30 Among useful changes in the backbone chemistry are phosphorothioates; phosphorodithioates, where both of the non-bridging oxygens are substituted with sulfur;

phosphoroamidites; alkyl phosphotriesters and boranophosphates. Achiral phosphate derivatives include 3'-O'-5'-S-phosphorothioate, 3'-S-5'-O-phosphorothioate, 3'-CH₂-5'-O-phosphonate and 3'-NH-5'-O-phosphoroamidate. Peptide nucleic acids replace the entire ribose phosphodiester backbone with a peptide linkage. Sugar modifications are also used to enhance stability and affinity. The α -anomer of deoxyribose may be used, where the base is inverted with respect to the natural β -anomer. The 2'-OH of the ribose sugar may be altered to form 2'-O-methyl or 2'-O-allyl sugars, which provides resistance to degradation without comprising affinity. Modification of the heterocyclic bases must maintain proper base pairing. Some useful substitutions include deoxyuridine for deoxythymidine; 5-methyl-2'-deoxycytidine and 5-bromo-2'-deoxycytidine for deoxycytidine. 5-propynyl-2'-deoxyuridine and 5-propynyl-2'-deoxycytidine have been shown to increase affinity and biological activity when substituted for deoxythymidine and deoxycytidine, respectively.

As an alternative to anti-sense inhibitors, catalytic nucleic acid compounds, *e.g.* ribozymes, anti-sense conjugates, *etc.* may be used to inhibit gene expression. Ribozymes may be synthesized *in vitro* and administered to the patient, or may be encoded on an expression vector, from which the ribozyme is synthesized in the targeted cell (for example, see International patent application WO 9523225, and Beigelman *et al.* (1995), *Nucl. Acids Res.* 23:4434-42). Examples of oligonucleotides with catalytic activity are described in WO 9506764. Conjugates of anti-sense ODN with a metal complex, *e.g.* terpyridylCu(II), capable of mediating mRNA hydrolysis are described in Bashkin *et al.* (1995), *Appl. Biochem. Biotechnol.* 54:43-56.

GENETICALLY ALTERED CELL OR ANIMAL MODELS FOR LGR4, LGR5 AND LGR7 FUNCTION

The subject nucleic acids can be used to generate transgenic, non-human animals or site specific gene modifications in cell lines. Transgenic animals may be made through homologous recombination, where the normal *LGR4*, *LGR5* or *LGR7* locus is altered. Alternatively, a nucleic acid construct is randomly integrated into the genome. Vectors for stable integration include plasmids, retroviruses and other animal viruses, YACs, and the like.

- The modified cells or animals are useful in the study of *LGR4*, *LGR5* and/or *LGR7* function and regulation. For example, a series of small deletions and/or substitutions may be made in the host's native *LGR4*, *LGR5* or *LGR7* gene to determine the role of different exons. Of interest is the use of *LGR4*, *LGR5* or *LGR7* to construct transgenic animal
- 5 models for disease states. Specific constructs of interest include anti-sense *LGR4*, *LGR5* or *LGR7*, which will block *LGR4*, *LGR5* or *LGR7* expression, expression of dominant negative *LGR4*, *LGR5* or *LGR7* mutations, and over-expression of *LGR4*, *LGR5* or *LGR7* genes. Where an *LGR4*, *LGR5* or *LGR7* sequence is introduced, the introduced sequence may be either a complete or partial sequence of an *LGR4*, *LGR5* or *LGR7* gene native to
- 10 the host, or may be a complete or partial *LGR4*, *LGR5* or *LGR7* sequence that is exogenous to the host animal, *e.g.*, a human *LGR4*, *LGR5* or *LGR7* sequence. A detectable marker, such as *lac Z* may be introduced into the *LGR4*, *LGR5* or *LGR7* locus, where upregulation of *LGR4*, *LGR5* or *LGR7* expression will result in an easily detected change in phenotype.
- 15 One may also provide for expression of the *LGR4*, *LGR5* or *LGR7* gene or variants thereof in cells or tissues where it is not normally expressed, at levels not normally present in such cells or tissues, or at abnormal times of development. By providing expression of *LGR4*, *LGR5* or *LGR7* protein in cells in which it is not normally produced, one can induce changes in cell behavior, *e.g.* through *LGR4*, *LGR5* or *LGR7* mediated activity.
- 20 DNA constructs for homologous recombination will comprise at least a portion of the *LGR4*, *LGR5* or *LGR7* gene, which may or may not be native to the species of the host animal, wherein the gene has the desired genetic modification(s), and includes regions of homology to the target locus. DNA constructs for random integration need not include regions of homology to mediate recombination. Conveniently, markers for
- 25 positive and negative selection are included. Methods for generating cells having targeted gene modifications through homologous recombination are known in the art. For various techniques for transfecting mammalian cells, see Keown *et al.* (1990), *Meth. Enzymol.* 185:527-537.

- For embryonic stem (ES) cells, an ES cell line may be employed, or embryonic
- 30 cells may be obtained freshly from a host, *e.g.* mouse, rat, guinea pig, *etc.* Such cells are grown on an appropriate fibroblast-feeder layer or grown in the presence of leukemia

inhibiting factor (LIF). When ES or embryonic cells have been transformed, they may be used to produce transgenic animals. After transformation, the cells are plated onto a feeder layer in an appropriate medium. Cells containing the construct may be detected by employing a selective medium. After sufficient time for colonies to grow, they are picked
5 and analyzed for the occurrence of homologous recombination or integration of the construct. Those colonies that are positive may then be used for embryo manipulation and blastocyst injection. Blastocysts are obtained from 4 to 6 week old superovulated females. The ES cells are trypsinized, and the modified cells are injected into the blastocoel of the blastocyst. After injection, the blastocysts are returned to each uterine horn of
10 pseudopregnant females. Females are then allowed to go to term and the resulting offspring screened for the construct. By providing for a different phenotype of the blastocyst and the genetically modified cells, chimeric progeny can be readily detected.

The chimeric animals are screened for the presence of the modified gene and males and females having the modification are mated to produce homozygous progeny. If the
15 gene alterations cause lethality at some point in development, tissues or organs can be maintained as allogeneic or congenic grafts or transplants, or in *in vitro* culture. The transgenic animals may be any non-human mammal, such as laboratory animals, domestic animals, etc. The transgenic animals may be used in functional studies, drug screening, etc., e.g. to determine the effect of a candidate drug on *LGR4*, *LGR5* or *LGR7* or related
20 gene activation etc.

IN VITRO MODELS FOR *LGR4*, *LGR5* or *LGR7* FUNCTION

The availability of a number of components in the G-protein coupled receptor family, as previously described, allows *in vitro* reconstruction of the processes or systems
25 in which members of this family operate. Two or more of the components, such as the isolated receptor and a potential ligand therefore, may be combined *in vitro*, and the behavior assessed in terms of activation of transcription of specific target sequences; modification of protein components, e.g. proteolytic processing, phosphorylation, methylation, etc.; ability of different protein components to bind to each other. The
30 components may be modified by sequence deletion, substitution, etc. to determine the functional role of specific domains.

Drug screening may be performed using an *in vitro* model, a genetically altered cell or animal, purified LGR4, LGR5 or LGR7 protein, as well as fragments or portions thereof, e.g. solubilized extra-cellular domain or chimeric receptor proteins comprising the LGR4, LGR5 or LGR7 extra-cellular domain. One can identify ligands or substrates that
5 bind to and modulate the action of LGR4, LGR5 or LGR7. Areas of investigation include the development of agents that beneficially counter abnormalities related to LGR4, LGR5 or LGR7 and the use of such agents in the therapy.

Drug screening identifies agents that modulate the activity of LGR4, LGR5 or LGR7 function in abnormal cells. Of particular interest are screening assays for agents
10 that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, and the like. The purified protein may also be used for determination of three-dimensional crystal structure, which can be used for modeling intermolecular interactions, such as GTP binding, *etc.*

15 The term "agent" as used herein describes any molecule, *e.g.* protein or pharmaceutical, with the capability of altering or mimicking the physiological function of LGR4, LGR5 or LGR7. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, *i.e.* at
20 zero concentration or below the level of detection.

In some embodiments, candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 daltons. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly
25 hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids,
30 purines, pyrimidines, derivatives, structural analogs or combinations thereof.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and oligopeptides. Alternatively, 5 libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means, and may be used to produce combinatorial libraries. Known pharmacological agents may be subjected to directed or random chemical modifications, 10 such as acylation, alkylation, esterification, amidification, *etc.* to produce structural analogs.

Of particular interest in certain embodiments are peptidic agents based on LGR4, LGR5 or LGR7, e.g. solubilized extra-cellular domain or chimeric receptor proteins comprising the LGR4, LGR5 or LGR7 extra-cellular domain, where such agents 15 neutralize the activity of endogenous LGR4, LGR5 or LGR7 ligands, e.g. hormones.

Where the screening assay is a binding assay, one or more of the molecules may be joined to a label, where the label can directly or indirectly provide a detectable signal. Various labels include radioisotopes, fluorescers, chemiluminescers, enzymes, specific binding molecules, particles, e.g. magnetic particles, and the like. Specific binding 20 molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin *etc.* For the specific binding members, the complementary member would normally be labeled with a molecule that provides for detection, in accordance with known procedures.

A variety of other reagents may be included in the screening assay. These include reagents like salts, neutral proteins, e.g. albumin, detergents, *etc.*, that are used to facilitate 25 optimal protein-protein binding and/or reduce non-specific or background interactions. Reagents that improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, *etc.*, may be used. The mixture of components are added in any order that provides for the requisite binding. Incubations are performed at any suitable temperature, typically between 4 and 40°C. Incubation periods are selected for 30 optimum activity, but may also be optimized to facilitate rapid high-throughput screening. Typically between 0.1 and 1 hours will be sufficient.

Other assays of interest detect agents that mimic LGR4, LGR5 or LGR7 function. For example, an expression construct comprising an *LGR4*, *LGR5* or *LGR7* gene may be introduced into a cell line under conditions that allow expression. The level of LGR4, LGR5 or LGR7 activity is determined by a functional assay, as previously described. In
5 one screening assay, the ability of candidate agents to inhibit or enhance LGR4, LGR5 or LGR7 function is determined. Alternatively, candidate agents are added to a cell that lacks functional LGR4, LGR5 or LGR7, and screened for the ability to reproduce LGR4, LGR5 or LGR7 activity in a functional assay.

The compounds having the desired pharmacological activity may be administered
10 in a physiologically acceptable carrier to a host for treatment, *etc.* The compounds may also be used to enhance *LGR4*, *LGR5* or *LGR7* function. The inhibitory agents may be administered in a variety of ways, orally, topically, parenterally *e.g.* subcutaneously, intraperitoneally, by viral infection, intravascularly, *etc.* Topical treatments are of particular interest. Depending upon the manner of introduction, the compounds may be
15 formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt.%.

The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and
20 topical use can be used to make up compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

25

EXPERIMENTAL

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the subject invention, and are not intended to limit the scope of what is regarded as the invention.
30 Efforts have been made to ensure accuracy with respect to the numbers used (*e.g.* amounts, temperature, concentrations, *etc.*) but some experimental errors and deviations

should be allowed for. Unless otherwise indicated, parts are parts by weight, molecular weight is average molecular weight, temperature is in degrees centigrade; and pressure is at or near atmospheric.

5 Example 1. Identification of LGR4 and LGR5

Human sequences related to the sea anemone and *Drosophila* glycoprotein hormone receptors were identified from the expression sequence tag database (dbEST) at the National Center for Biotechnology Information by using the BLAST server with the BLOSUM62 protein comparison matrix (Altschul SF *et al*, Nucleic Acids Res (1997)
10 25:3389-3402). Human ESTs showing high homology to two non-overlapping regions of the gonadotropin receptors were identified. Clones AA312798 and AA298810 were found to encode transmembrane four to five of the putative receptor LGR4 whereas AA460529 and AA424098 encode transmembrane two to three of the putative receptor LGR5. Using these ESTs to further search the GenBank EST division database,
15 overlapping EST sequences were aligned to obtain the longest open reading frame (ORF) for these receptors.

Based on the longest human ORF, specific primers were designed for PCR amplification of LGR4 and LGR5 cDNA fragments from rat ovary and human placenta, respectively. After hybridization with labeled EST clones and confirmation of DNA
20 sequences by dideoxy DNA sequencing, specific receptor fragments isolated were used to design primers to prepare sub-cDNA libraries enriched with specific receptor cDNAs. For 5' extension, reverse transcription was performed using rat ovarian and human placenta mRNA preparations and receptor-specific primers. Following second strand synthesis, the enriched cDNA pool was tailed at 5'-ends with specific adaptor sequences to allow further
25 PCR amplification. For 3' extension, rat ovarian or human placenta mRNAs were reversed transcribed using oligo-dT, followed by second strand synthesis using receptor-specific primers and adaptor tailing. These mini-libraries were further used as templates for PCR amplification of upstream or downstream cDNAs specific for each receptor using internal primers. PCR products with a strong hybridization signal to each receptor cDNA
30 fragment were subcloned into the pUC18 or pcDNA3 vectors. After screening of these sublibraries based on colony hybridization using specific receptor probes, clones with 5'-

or 3'-sequences of the putative receptors were identified and isolated for DNA sequencing. As needed, the procedure was repeated up to three times to generate cDNAs encoding the complete ORF of each putative receptor for sequence analysis and for the expression of receptor proteins in eukaryotic cells. The entire coding sequences of each
5 gene were also amplified with specific primers flanking the entire ORF in independent experiments. At least three independent PCR clones were sequenced to verify the authenticity of coding sequences. The nucleotide sequence of LGR4, as well as the amino acid sequence of the product encoded by the ORF thereof, is provided in Fig. 1. The nucleotide sequence of LGR5, as well as the amino acid sequence of the product encoded
10 by the ORF thereof, is provided in Fig. 2.

Example 2. Comparison of deduced amino acid sequence of LGR4 and 5 cDNAs and those encoding FSH and LH receptors.

15 Sequence alignment of LGR4 and LGR5 with known human glycoprotein hormone receptors was performed and the results are shown in Fig. 6. Shaded residues are identical in at least two of the four receptor proteins shown.

Example 3. Expression pattern of LGR4 and 5 mRNA transcripts in different tissues.
20

For northern blot analysis, poly (A)+-selected RNA from different human tissues was hybridized with a ³²P-labeled cDNA probes. After washing, the blots were exposed to X-ray films at -70C for five days. Subsequent hybridization with a beta-actin cDNA
25 probe was performed to estimate nucleic acid loading (8 h exposure). LGR4 was shown to be expressed in placenta, ovary, testis, adrenal, spinal cord, thyroid, stomach, trachea, heart, pancreas, kidney, prostate and spleen while LGR5 was shown to be expressed in the skeletal muscle, placenta, spinal cord, brain, adrenal, colon, stomach, ovary and bone marrow.

30

Example 4. Chromosomal localization of LGR4 and 5 in human.

Using genomic fragments of LGR4 (>100 Kb) and LGR5 (>100 Kb) as probes, chromosomal localization of these genes were detected using the FISH method to banded DNA in chromosomal 5q34-35.1 and 12q15, respectively.

5

Example 5. Identification of LGR7.

Analysis of EST databases has revealed a novel LGR closely related to a G protein-coupled receptor from pond snail (*Lymnaea stagnalis*, accession no. 481946). Because the snail G-protein coupled receptor shared the leucine-rich repeat ectodomain and seven
10 transmembrane region characteristics of mammalian LGRs, the novel EST sequence could encode either a homologue of snail receptor or a novel mammalian LGR. For the isolation of LGR7 cDNA, a Clontech Marathon-ready testis cDNA pool was used as the template for 5' and 3' RACE with adapter and gene-specific primers. Sequence analysis of the RACE products showed that LGR7 gene encode at least two splicing variants differ at the N-
15 terminus. The nucleotide sequence of the long variant, as well as the amino acid sequence of the product encoded by the ORF thereof, is provided in Fig. 3; while the nucleotide sequence of the short variant, as well as the amino acid sequence of the ORF thereof, is provided in Fig. 4. Both variants contain a classical C-terminal 7-transmembrane region and a leucine-rich repeat ectodomain flanked by cysteine rich regions found in other mammalian LGRs. The
20 long form LGR7 contains extra 35 amino acids in the N-terminal cysteine rich region as compared to the short form LGR7. Of interest, analysis of the LGR7 ORF from either variant showed that its tertiary structure resembles that of mammalian LGRs instead of the snail receptor, which shares the greatest identity in the transmembrane region. These findings suggest that LGR7 and snail receptor diverged early during evolution and LGR7 perhaps
25 adopted new function in higher organisms.

Based on the LGR7 cDNA sequence, we further identified a human genomic DNA fragment (AQ053279) in the genomic survey sequence division of GenBank that contains part of the LGR7 gene. The authenticity of this genomic clone was confirmed by Southern blot hybridization and the genomic clone was used as the probe to identify the
30 chromosomal localization for LGR7 gene.

It is evident from the above discussion and results that three novel mammalian G-protein coupled receptors, as well as a nucleic acids encoding the same, are provided by the subject invention. The inventions described above find use in a variety of applications, including research and therapeutic applications.

5

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such a disclosure by virtue of prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

WHAT IS CLAIMED IS:

1. An isolated nucleic acid encoding a mammalian protein selected from the group consisting of LGR4, LGR5 or LGR7.
5
2. An isolated nucleic acid according to Claim 1, wherein said mammalian protein has the amino acid sequence of SEQ ID NO:2, SEQ ID NO:04, SEQ ID NO:06 or SEQ ID NO:08.
- 10 3. An isolated nucleic acid according to Claim 1, wherein said mammalian protein has an amino acid sequence that is substantially identical to the amino acid sequence of SEQ ID NO:2, SEQ ID NO:04, SEQ ID NO:06 or SEQ ID NO:08.
4. An isolated nucleic acid according to Claim 1, wherein the nucleotide
15 sequence of said nucleic acid has the sequence selected from the group consisting of: (a) SEQ ID NO:1 or the complementary sequence thereof; (b) SEQ ID NO:03 or the complementary sequence thereof; (c) SEQ ID NO:05 or the complementary sequence thereof; and (d) SEQ ID NO:07 or the complementary sequence thereof.
- 20 5. An isolated nucleic acid comprising at least 18 contiguous nucleotides of the sequence selected from the group consisting of: (a) SEQ ID NO:1 or the complementary sequence thereof; (b) SEQ ID NO:03 or the complementary sequence thereof; (c) SEQ ID NO:05 or the complementary sequence thereof; and (d) SEQ ID
25 NO:07 or the complementary sequence thereof.
6. An isolated nucleic acid comprising at least 50 contiguous nucleotides of the sequence selected from the group consisting of: (a) SEQ ID NO:1 or the complementary sequence thereof; (b) SEQ ID NO:03 or the complementary sequence thereof; (c) SEQ ID NO:05 or the complementary sequence thereof; and (d) SEQ ID
30 NO:07 or the complementary sequence thereof.

7. An isolated nucleic acid that hybridizes under stringent conditions to a nucleic acid having the nucleotide sequence selected from the group consisting of: (a) SEQ ID NO:1 or the complementary sequence thereof; (b) SEQ ID NO:03 or the
5 complementary sequence thereof; (c) SEQ ID NO:05 or the complementary sequence thereof; and (d) SEQ ID NO:07 or the complementary sequence thereof.

8. An expression cassette comprising a transcriptional initiation region functional in an expression host, a nucleic acid having a sequence of the isolated nucleic
10 acid according to Claim 1 under the transcriptional regulation of said transcriptional initiation region, and a transcriptional termination region functional in said expression host.

9. A cell comprising an expression cassette according to Claim 8 as part of an
15 extrachromosomal element or integrated into the genome of a host cell as a result of introduction of said expression cassette into said host cell, and the cellular progeny of said host cell.

10. A method for producing a mammalian protein selected from the group
20 consisting of LGR4, LGR5 and LGR7, said method comprising:
growing a cell according to Claim 9, whereby said mammalian protein is expressed; and
isolating said protein substantially free of other proteins.

25 11. A purified polypeptide composition comprising at least 50 weight % of the protein present as a mammalian protein selected from the group consisting of LGR4, LGR5 and LGR7, or a fragment thereof.

12. An antibody binding specifically to a mammalian protein selected from the
30 group consisting of LGR4, LGR5 and LGR7.

13. The antibody of Claim 12, wherein said antibody is a monoclonal antibody.

14. A non-human transgenic animal model for *LGR4*, *LGR5* or *LGR7* gene function, wherein said transgenic animal comprises an introduced alteration in an *LGR4*,
5 *LGR5* or *LGR7* gene.

15. The animal model of claim 14, wherein said animal is heterozygous for said introduced alteration.

10 16. The animal model of claim 14, wherein said animal is homozygous for said introduced alteration.

17. The animal model of claim 14, wherein said introduced alteration is a knockout of endogenous *LGR4*, *LGR5* or *LGR7* gene expression.

15

18. A method of screening a sample for the presence of a ligand for a receptor selected from the group consisting of *LGR4*, *LGR5* and *LGR7*, said method comprising:
contacting said sample with a receptor selected from the group consisting of *LGR4*, *LGR5* and *LGR7* or a mimetic thereof, and

20 detecting the presence of a binding event between said receptor and ligand in said sample.

>LGR4 nucleotide sequence (SEQ ID NO:01)

ATGCCGGGCGCTAGGGCTGCTCTGCTTCCTCGCCCTGGGGCTGCTCGGCTCGGCCGGGCCCCAGCGGCGCGGCGCCGCCT
CTCTGCGCGGCGCCCTGCAGCTGCGACGGCGACCGTCGGGTGGACTGCTCCGGAAAGGGGTTGACGGCCGTACCGGAGGGT
CTCAGCGCCTTCACCAAGCACTGGATATCAGTATGAACAATATCACCCAGTTACCAGAAGATGCATTTAAGAGTTTCCCA
TTTCTAGAGGAGCTACAACCTGGCTGGTAACGACCTTTCTCTTATCCATCCAAAAGCCTTGCTGGGCTGAAAGAACTCAA
GTCCTAACACTCCAGAATAATCAGTTGAGAACAGTGCCAGTGAAGCCATTACGCGACTGAGTGCCTTTGCAGTCTTTACGC
TTAGATGCCAACCATATTACCTCAGTCCCGGAGGACAGTTTTGAAGGGCTTGTCAGTTACGCCATCTGTGGCTGGATGAC
AACAGCTTGACGGAAGTGCCCGTGCGTCCCCTCAGCAACCTGCCAACCTGCAGGCGCTGACCTTGGCTCTCAACAACATC
TCAAGCATCCCTGACTTCGCTTTACCAACCTTTCAAGCTTGGTGGTCTGTCATCTGCATAACAATAAAATTTAAAGCCTC
AGTCAACACTGTTTTGATGGACTAGATAACCTGGAACCTTGGACTTGAATTACAATTACTTGGATGAGTTTCTCAGGCT
ATTAAAGCCCTTCCAGCCTTAAAGAGCTGGGATTTACAGTAATTCTATTTCTGTTATTCTGATGGAGCATTGGTGGT
AATCCACTGCTAAGAACTATTCAATTTGATGATAATCCTCTGCTTTTGTGGGGAACCTCAGCATTTCAACCTGTCTGAT
CTGCATTGCTTAGTCATTTCGTGGTGCAAGCCTGGTGCACTGGTTCCTCAATCTGACCGGAACCTGTCATTGGAGAGTCTA
ACCTTGACAGGGACAAAAATAAGCAGCATACCTGATGATCTGTGCCAAAACCAAAAGATGCTGAGGACTCTGGACTTATCT
TATAACAATATAAGAGACCTTCCAAGTTTAAATGGTGTGCTGCATTGGAAGAAATTTATTGCAGCGTAATCAAATCTCC
CTAATAAAGGAAAAATCTTTTCAAGGCCTAACATCTCAAGGATCTAGATTGAAGTTTCAATGAATTAACCTTATTTCCTACGGAAGGC
AGTGGAGCTTTTGCAGAGCTTGGGACAATTAACTGAGTGAAGTTTCAATGAATTAACCTTATTTCCTACGGAAGGC
CTAATGGGCTCAATCAACTAAAGCTTGTGGGTAACCTCAAGCTGAAAGACGCTTGGCAGCCAGAGACTTTGCTAATCTC
AGGTCTCTATCAGTACCATATGCTTATCAGTGTGTGCAATTTTGGGGGTGTGACTCTTTATGCAAAATAACACAGAAGAT
AACAGCCCCCAAGAACACAGTGTGACAAAAGAGAAAGGTGCTACAGATGCAGCAAATGTCACCAGCACTGCTGAGAACGAA
GAACATAGCCAAATAATTATCCACTGTACACCTTCAACAGGTGCTTTCAAGCCCTGTGAATATTTACTGGGAAGCTGGATG
ATTGCGCTTACAGTGTGGTTTCAATTTCTGCTGCGCTTGTCTTTCAACCTGCTTGTCAATTTTACAGTGTTCGCTCTTGT
TCATCACTGCCTGCCTCCAACTCTTCATAGGCTTGATTTCTGTGCTAACTTACTCATGGGCATCTATACTGGCATCCTT
ACTTTTCTTGATGCTGTGCTCTGGGGCCGATTTGCCGAATTTGGCATTGGTGGGAACTGGCAGCGGCTGCAAGGTAGCC
GGTCTCTGGCAGTCTTCTCCTCAGAGAGCGCTGATTCTTAACTGGCAGCTGTGGAAGAAGCGTATTGCAAAG
GATTTGATGAAACACGGGAAGAGCAGTCACCTCAGACAGTTCCAGGTGGCCGCCCTCTTAGCTTTGCTGGGTGCCGAGTG
GCAGGCTGCTTCCCCCTTTTCCACGGAGGGCAATATTCTGCATCGCCCTTGTGTTTGCCTTTCTACAGGAGAAACCCCA
TCGTTAGGATTCAGTGTGACCTTAGTGCTATTAACCTCACTGGCATTTTTACTAATGGCCATTATCTACACTAACTATAC
TGCAACTTAGAGAAGGAGGACCTGTGCGAAAACCTCCAGTCTAGCGTGATTAAGCACGTTGCTGGCTCATCTTCACAAAC
TGCATCTTCTTCTGCGCTGTTGCATTTTCTCATTGACCATTTGATCACGGCAATCTCCATCAGCCCCGAGATAATGAAG
TCTGTTACACTGATATTCTTCCCGTTGCCTGCTTGCCTGAATCCGGTCTGTATGTTTTCTTCAACCCAAAGTTTAAAGAA
GACTGGAAGCTACTGAAGCGGCGTGTACCAGGAAACACGGATCTGTTTCACTTCCATCAGCAGCCAAGCGGTTGTGGG
GAACAGGATTTCTACTATGACTGTGGCATGTATCCCACTTGCAGGGTAACCTGACTGTCTGTGACTGCTGTGAGTCATT
CTTTTGACAAAACAGTATCATGCAACACTTAATAAAATCGCACAGTTGTCTGTATTGACAGCGGCCTTGTGCCAGAGG
CCAGAGCCTTACTGGTCTGATTGTGTACACAGTCAGCCCATTTGACTATGCAGATGAAGAAGATTCTTTGTCTCAGAC
AGCTCTGACCAGGTGCAGGCCTGTGGACGAGCCTGCTTCTACCAGAGTCGTGGATTCCCTCTGGTGCCTATGCTTACAAT
CTACAGAGAGTCAGAGACTGA

>LGR4 amino acid sequence (SEQ ID NO:02)

MPGPLGLLCFLALGLLGSAGPSGAAPPLCAAPCSDGDRRVDCSGKGLTAVPEGLSAFTQALDISMNNITQLPEDAFKSF
FLEELQLAGNDLSLIHPKALSGLKELKVLTLQNNQLRTVPSEAIHGLSALQSLRLDANHITSVPEDSFEGVLQRLHLWDD
NSLTVVPVRPLSNLPTLQALTALNLISSIPDFAFTNLSSLVVLHLHNNKIKSLSQHCFDGLDNLETDLNLYNYLDEFPOA
IKALPSLKELGFHSNSISVIPDGAFGGNPLLRTHLYDNPLSFVGNLSAFHNLSDLHCLVIRGASLVQWFPNLGTGVHLESL
TLTGTKISSIPDDLQCNQKMLRTLDSLNNIRDLPSFNGCRALEELSLQRNQISLIKENTFQGLTSLRILDLNRNLIREIH
SGAFALGTLITNLDVSFNELTSPTEGLNGLNQLKLVGNFKLDALAARDFANLRSLVPHYAYQCCAFWGCDSLCKLNTED
NSPQEHVSVTEKGATDAANVTSTAENEHSQIIHCTPSTGAFKPCYLLGSWMIRLTVWFI FLVALLFNLLVILTVFASC
SSLPASKLFI GLISVSNLLMGIYTGILTFDAVSWGRFAEFGIWWETGSGCKVAGSLAVFSSES AVFLLTLAAVERSVFAK
DLMKHGKSSHRLRQFVAALLALLGA AVAGCFPLFHGGQYSASPLCLPFPTGETPSLGFTVTLVLLNSLAFLLMAI IYTKLY
CNLEKEDLSENSQSSVIKHWAWLIFTNCFECPVAFSSFAPLITAISSPEIMKSVTLIFFPLPACLPVLYVFFNPKFKE
DWKLLKRRVTRKHGSVSVSISSQGGCGEQDFYDCGMYSHLQGNLTVCDCESFLLTKPVSKHLIKSHSCPVLTAASCQR
PEAYWSDCGTQSAHSDYADEEDSFVSDSSDQVQACGRACFYQSRGFPLVRYAYNLQVRD

FIG. 1

>Nucleotide sequence of LGR5 (total 2082 nucleotides) (SEQ ID NO:03)

CTACATCTCCATAACAATAGAATCCACTCCCTGGGAAAGAAATGCTTTGATGGGCTCCACAGCCTAGAGACTTTAGATTTA
AATTACAATAACCTTGATGAATTCCCCACTGCAATTAGGACACTCTCCAATTAAAGGAACTAGGATTTATAGCAACAAT
ATCAGGTCGATACCTGAGAAAGCATTGTAGGCAACCTTCTCTTATTACAATACATTTCTATGACAAATCCCATCCAATTT
GTTGGGAGATCTGCTTTTCAACATTTACCTGAACTAAGAACACTGACTCTGAATGGTGCCTCAGAAATAACTGAATTTCTT
GATTTAACTGGAACCTGCAACCTGGAGAGTCTGACTTTAACTGGAGCACAGATCTCATCTCTTCTCAAACCGTCTGCAAT
CAGTTACCTAATCTCCAAGTGCTAGATCTGTCTTACAACCTATTAGAAGATTTACCCAGTTTTTTCAGTCTGCCAAAGCTT
CAGAAAATTGACCTAAGACATAATGAAATCTACGAAATTAAGATTGACACTTTCCAGCAGTTGCTTAGCCTCCGATCGCTG
AATTTGGCTTGGAACAAAATTGCTATTATTACCCCAATGCATTTTCCACTTTGCCATCCCTAATAAAGCTGGACCTATCG
TCCAACCTCCTGTCGTCTTTTCTATAACTGGGTTACATGGTTTAACTCACTTAAAATTAACAGGAAATCATGCCTTACAG
AGCTGGATATCATCTGAAAACCTTTCCAGAACTCAAGGTATAGAAATGCCTTATGCTTACCAGTGTCTGTCATTTGGAGTG
TGTGAGAATGCCTATAAGATTTCTAATCAATGGAATAAAGGTGACAACAGCAGTATGGACGACCTTCATAAGAAAGATGCT
GGAATGTTTCAGGCTCAAGATGAACGTGACCTTGAAGATTTCTGCTTGACTTTGAGGAAGACCTGAAAGCCCTTCAATCA
GTGCAGTGTTACCTTCCCCAGGCCCTTCAAACCTGTGAAACCTGCTTGATGGCTGGCTGATCAGAATTGGAGTGGG
ACCATAGCAGTTCTGGCACTTACTTGTAAATGCTTTGGTGACTTCAACAGTTTTCAGATCCCTCTGTACATTTCCCCCATT
AAACTGTTAATTGGGGTCATCGCAGCAGTGAACATGCTCACGGGAGTCTCCAGTGCCGTGCTGGCTGGTGTGGATGCGTTC
ACTTTTGGCAGCTTTGCACGACATGGTGCCTGGTGGGAGAATGGGGTTGGTTGCCATGTCATTGGTTTGTGTCATTTT
GCTTCAGAAATCATCTGTTTCTGCTTACTCTGGCAGCCCTGGAGCGTGGGTTCTCTGTGAAATATTCTGCAAAATTTGAA
ACGAAAGCTCCATTTTCTAGCCTGAAAGTAATCATTTTGTCTGTGCCCTGCTGGCCTTGACCATGGCCGAGTTCCTCTG
CTGGGTGGCAGCAAGTATGGCGCCTCCCTCTCTGCTGCTTGGCTTTTGGGGAGCCAGCACCATGGGCTACATGGTC
GCTCTCATCTTGCTCAATTTCCCTTTGCTTCTCATGATGACCATTGCCCTACACCAAGCTCTACTGCAATTTGGACAAGGGA
GACCTGGAGAATATTTGGGACTGCTCTATGGTAAACACATTGCCCTGTTGCTCTTACCAACTGCATCTAAACTGCCCT
GTGGCTTTCTGTCTCTCTCTCTTTAATAAACCTTACATTTATCAGTCTGAGTAATTAAGTTTATCTTCTGGTGGTA
GTCCCACTTCTGTCATGTCTCAATCCCTTCTCTACATCTTGTCAATCCTCACTTTAAGGAGGATCTGGTGAGCCTGAGA
AAGCAAACCTACGTCTGGACAAGATCAAAACACCAAGCTTGTATGTCAATTAACCTGATGATGTCGAAAAACAGTCTGT
GACTCAACTCAAGCCTTGTAACCTTTACCAGCTCCAGCATCACTTATGACCTGCCTCCAGTTCCGTGCCATCACCAGCT
TATCCAGTGACTGAGAGCTGCCATCTTCTCTGTGGCATTGTGCCATGTCTCTAA

>amino acid sequence of LGR5 (total 693 amino acids) (SEQ ID NO:04)

LHLHNNRIHSLGKKCFDGLHSLETLDLNNNLDEFPTAIRTLNKLKELGFHSSNNIRSIPKAFVGNPSLTIHFYDNPFIQF
VGRSAFQHLPELRITLTLNGASQITEFPDLTG TANLESLLTGAQISSLPQTVCNQLPNLQVLDLSYNLLEDLPFSVCQKL
QKIDLRHNEIYEIKVDTFQQLSLRSLNLAWNKIAIIHPNAFSTLP SLIKL DLSSNLLSSFPITGLHGLTHLKL TGNHALQ
SWISSENFPELKVIEMPYAYQCCAFGVCENAYKISNQWNKGDNSSMDDLHKRDAGMFAQQDERDLEDFLD FEEDLKALHS
VQCSPPSPGPFKPEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIAAVNMLTGVS SAVLAGVDAF
TFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLTLAALERGF SVKYS AKFETKAPFSSLKVI ILLCALLAL TMAAVPL
LGGSKYGASPLCLPLPFGEPSMTGYMVALILLNSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCIILNCP
VAFLSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNP HFKEDLVSLRKQTYVWTRSKHPSLMSINSDDVEKQSC
DSTQALVTFTSSSITYDLPPSSVPSPAYPVTESCHLSSVAFVPC L

FIG. 2

>Final LGR7 (LGR7-Long variant) full length sequence (2467 nt) (SEQ ID NO:05).

GAAAGGAGGAAAGAAAAAGAGGAATGGAAAGAGACAGAGAAAGGAATGGGAGTGGAGGAGGAGGACTGCTTT
GTAACGTCTAAGATTGCAGACAGAAATAGCACACAACCACTGTGAGCTGTATGCGATTGAGAAACCAAGACCAAATT
TTGCTCACTTTTCATTAATCAGTTGCTCAGATAGAAGGAAATGACATCTGGTTCTGTCTTCTTCTACATCTTAATTTT
TGGAAAATATTTTTCTCATGGGGGTGGACAGGATGTCAAGTGCTCCCTTGGCTATTTCCTTGTGGGAACATCACAA
AGTGCTTGCTCAGCTCCTGCACTGTAACGGTGTGGACGACTGCGGGAATCAGGCCGATGAGGACAACTGTGGAGAC
AACAATGGATGGTCCATGCAATTTGACAAATATTTTGCAGTTACTACAAAATGACTTCCCAATATCTTTTGGAGC
AGAAACACCTGAATGTTTGGTCGGTCTGTGCCAGTGCAATGTCTTTGCCAAGGTCTGGAGCTTGACTGTGATGAAA
CCAATTTACGAGCTGTTCCATCGGTTTCTTCAAATGTGACTGCAATGTCACTTCAGTGGAACTTAATAAGAAAGCTT
CCTCCTGATGCTTCAAGAAATATCATGATCTTCAGAACTGTACCTGCAAAACAATAAGATTACATCCATCTCCAT
CTATGCTTTTCAGAGGACTGAATAGCCTTACTAACTGTATCTCAGTCATAACAGAATAACCTTCCTGAAGCCGGGTG
TTTTTGAAGATCTTCACAGACTAGAATGGCTGATAATTGAAGATAATCACCTCAGTCGAATTTCCCCACCAACATTT
TATGGACTAAATCTCTTATTCTCTTAGTCTGTGATGAATAACGTCTCACCCTTTACCTGATAAACCTCTCTGTCA
ACACATGCCAAGACTACATTGGCTGGACCTTGAAGGCAACCATATCCATAATTTAAGAAATTTGACTTTTATTTCTCT
GCAGTAATTTAACTGTTTTAGTGATGAGGAAAAACAAATTAATCACTTAAATGAAAAATACTTTTGACCTCTCCAG
AACTGGATGAATTTGATTTAGGAAGTAATAAGATTGAAAAATCTTCCACCGCTTATATTCAAGGACCTGAAGGAGCT
GTCACAATGAATCTTTCTTATAATCCAATCCAGAAAATTCAAGCAAACCAATTTGATTATCTTGTCAAACCTCAAGT
CTCTCAGCTAGAAGGGATTGAAATTTCAAATATCCAACAAAGGATGTTTAGACCTTTATGAATCTCTCTCACATA
TATTTTAAAGAAATCCAGTACTGTGGGTATGCACCACATGTTCCGAGCTGTAAACCAAACTGATGGAATTTTCATC
TCTAGAGATCTCTTGGCAAGCATTATTAGAGAGTATTTGTCTGGGTGTATCTGCAGTTACCTGCTTTGGAACA
TTTTTGTCAATTTGCATGCGACCTTATATCAGGTCTGAGAACAAGCTGTATGCCATGTCAATATTTCTCTCTGCTGT
GCCGACTGCTTAATGGGAATATATTTATTCGTGATCGGAGGCTTTGACCTAAAGTTTCGTGGAGAATACAATAAGCA
TGCGCAGCTGTGGATGGAGAGTACTCATTGTGAGTATCTTTGGCCATTCTGTCCACAGAAGTATCAGTTT
TACTGTTTAACTTTCTGACATTGGAATAATACATCTGCATTGTCTATCCTTTTAGATGTGTGAGACCTGGAATAATGC
AGAACAATTACAGTTCTGATTCTCATTGGATTACTGGTTTTATAGTGGCTTTCATTCCATTGAGCAATAAGGAATT
TTTCAAAACTACTATGGCACCATGGAGTATGCTTCCCTCTTCACTCAGAAGATACAGAAAGTATTGGAGCCCAGA
TTTATTCACTGGCAATTTTCTTGGTATTAATTTGGCCGATTTATCATCATAGTTTTTCTTATGGAAGCATGTTT
TATAGTGTTCATCAAAGTGCCATAACAGCAACTGAAATACGGAATCAAGTTAAAAAGAGATGATCCTTGCCAAACG
TTTTTTCTTTATAGTATTACTGATGCATTATGCTGGATACCCATTTTGTAGTGAAATTTCTTTCACTGCTTCAGG
TAGAAATACCAGGTACCATTAACCTCTTGGGTAGTGATTTTATTCTGCCCATTAAACAGTGCTTTGAACCCAAATCTC
TATACTCTGACCACAAGACCATTAAAGAAATGATTCATCGGTTTTGGTATAACTACAGACAAAGAAAATCTATGGA
CAGCAAAGGTCAGAAAACATATGCTCCATCATTATCTGGGTGGAAATGTGGCCACTGCAGGAGATGCCACCTGAGT
TAATGAAGCCGGACCTTTTACATACCCCTGTGAAATGTCACTGATTTCTCAATCAACGAGACTCAATTCCTATTCA
TGA

>Final LGR7 (LGR7-long variant, total 757 amino acids)(SEQ ID NO:06)

MTSGSVFFYILIFGKYFSGGGQDVKCSLGYFPCGNITKCLPQLLHCNGVDDCGNQADEDNCGDNNGWSMQFDKYFA
SYKMTSQYPFEAETPECLVGSVPVQCLCQGLELDDETNLRAPVSVSSNVTAMSLQWNLIRKLPDPDCFKNYHDLQK
LYLQNNKITSISIIYAFRGLNSLTCLYLHSHNRITFLKPGVFEDLHRLLEWLIIEDNHLRSISPPTFYGLNSLILLVLMN
NVLTRLPDKPLCQHMPRLHWDLEGNHINLRNLTFISCSNLTVLVMRKNKINHLNENTFAPLQKLDELDSLGNKIE
NLPLIFKDLKELSQLNLSYNPIQKIQANQFDYLVKLSLSLEGIEISNIQRMFRPLMNLSHIYFKKFQYCGYAPH
VRSCPNNTDGISSLENLLASIIQRVFVWVSAVTCFNIIFVICMRPYIRSENKLYAMSIIISLCCADCLMGIYLFVIG
GFDLKFGEYNKHAQLWMESTHCQLVGLAILSTEVSVLLLTFLTLEKYICIVYPPRCVRPGKCRITITVLILIWITG
FIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINLAAFIIVFSYGSMPFSVHQSAITATEI
RNQVKKEMILAKRFFFIIVFTDALCWIPIFVVKFLSLLQVEIPGTITSWVVIIFILPINSALNPILYTLTTRPFKEMIH
RFWYNRQRKSMDSKGQKTYAPSFIVWEMWPLQEMPPELMKPDLTFTYPEMSLISQSTRLNSYS*

FIG. 3

>Final LGR7 (LGR7-Short variant) full length sequence (3584 nt)(SEQ ID NO:07)

CTGCTTTGTAAGTCTAAGATTGCAGACAGAAATAGCACACAACCACTGTGAGCTGTATGCCGATTGAGAAACCAAGA
 CCAAATTTTGCTCACTTTTCATTAATCAGTTGCTCAGATAGAAGGAAATGACATCTGGTTCTGTCTTCTTCTACATCT
 TAATTTTGGAAAAATATTTTCTCATGGGGGTGGACAGGATGTCAAGTGCTCCCTTGGCTATTTCCCTGTGGGAAC
 ATCACAAGTGCTTGCTCAGCTCCTGCACTGTAAACGGTGTGGACGACTGCGGGAATCAGGCCGATGAGGACAACTG
 TGTGGTGGTTTTGTGCCAGTGCATGCTTTGCCAGGTCTGGAGCTTGAAGTGAAGAACATTACGAGTGTCCAT
 CGGTTTTCTCAAATGTGACTGCAATGTCACTTCAGTGGAACCTAATAAGAAAGCTTCTCCTGATTGCTTCAAGAAT
 TATCATGATCTTCAGAAGCTGGACCTGCAAAACAATAAGATTACATCCATCTCCATCTATGCTTTCAGAGGACTGAA
 TAGCCTTACTAACTGTATCTCAGTCATAACAGAATAACCTTCTGAAGCCGGGTGTTTTTGAAGATCTTCACAGAC
 TAGAATGGCTGACAAATGAAGATAATCACCTCAGTCGAATTTCCCAACCAACATTTTATGGACTAAATCTCTTATT
 CTCTTGTCTGATGAATAACGCTCCTCACCCGTTTACCTGATAAACCTCTCTGTCAACACATGCCAAGACTACATTG
 GCTGGACCTTGAAGGCAACCATATCCATAATTTAAGAAATTTGACTTTTATTTCTGTCAGTAATTTAACTGTTTTAG
 TGATGAGGAAAAACAAAATTAATCACTTAAATGAAAATACTTTTGACCTCTCCAGAACTGGATGAATGGATTTA
 GGAAGTAATAAGATTGAAAATCTTCCACCGCTTATATTCAAGGACCTGAAGGAGCTGTACAAATTGAATCTTTCCTA
 TAATCCAATCCAGAAAATTCAGCAACCAATTTGATTATCTTGTCAAACCTCAAGTCTCTCAGCCTAGAAGGGATTG
 AAATTTCAAATATCCAACAAAGGATGTTTAGACCTCTTATGAATCTCTCTCACATATATTTTGAAGAAATTCAGTAC
 TGTGGGTATGCACCATGTTTCGCAGCTGTAAACCAACATGATGGAATTTATCTCTAGAGAATCTCTTGGCAAG
 CATTATTCAGAGAGTATTTGTCTGGGTTGTATCTGCAGTTACCTGCTTTGGAACATTTTTTGTCAATTTGCATGCGAC
 CTTATATCAGGTCTGAGAACAGCTGTATGCCATGTCAATCATTTCTCTGCTGTGCGGACTGCTTAATGGGAATA
 TATTTATTCGTGATCGGAGGCTTTGACCTAAAGTTTCGTGGAGAATACAATAAGCATGCGCAGCTGTGGATGGAGAG
 TACTCATTGTGAGCTTGTAGGATCTTTGGCCATTCTGTCCACAGAAGTATCAGTTTTACTGTTAAACATTTCTGACAT
 TGGAAAAATACATCTGCATTGTCTATCCTTTTAGATGTGTGAGACCTGGAATAATGCAGAACAAATACAGTTCTGATT
 CTCATTGGATTACTGGTTTTATAGTGGCTTTTCAATTCAGCAATAAGGAATTTTTCAAAAATCTATATGGCAC
 CAATGGAGTATGCTTCCCTCTTCATTCAGAAGATACAGAAAGTATTGGAGCCAGATTTATTCAGTGGCAATTTTTT
 TTGGTATTAATTTGGCCGCATTTATCATCATAGTTTTTCTTATGGAAGCATGTTTTATAGTGTTCATCAAAGTGCC
 ATAACAGCAACTGAAATACGGAATCAAGTTAAAAAGAGATGATCCTTGCCAAACGTTTTTCTTTATAGTATTTAC
 TGATGCATTATGCTGGATACCCATTTTGTAGTGAAATTTCTTTCACTGCTTCAGGTAGAAATACCAGGTACCATAA
 CCTCTTGGGTAGTGATTTTTATTCTGCCCATTAACAGTGCTTTGAACCAATTTCTCTATCTCTGACCACAAGACCA
 TTTAAAGAAATGATTATCGGTTTTTGGTATAACTACAGCAAGAAAAATCTATGGACAGCAAGGTGAGAAAACATA
 TGCTCCCATTCATTCATGGGTGGAATGTGGCCACTGAGGAGATGCCACCTGAGTTAATGAAGCCGACCTTTTCA
 CATAACCCCTGTGAATGTCACTGATTTCTCAATCAACGAGACTCAATTCCTATTCATGACTGACTCTGAAATTCATT
 TCTTCGCAGAGAATACTGTGGGGGTGCTTCATGAGGGATTTACTGGTATGAAATGAATACCACAAAATTAATTTAT
 AATAATAGCTAAGATAAATATTTTACAAGGACATGAGGAAAAATAAAAATGACTAATGCTCTTACAAAGGGAAGTAA
 TTATATCAATAATGTATATATATTAGTAGACATTTTGCATAAGAAATTAAGAGAAATCTACTTCAGTAACATTCATT
 CATTTTTCTAACATGCATTTATTGAGTACCCACTACTATGTGCATAGCATTGCAATATAGTCTGGAAGTAGACAGT
 GCAGAACCTTTCAATCTGTAGATAGTGTTTAATGACAAAAGACTATACAAAGTCCATCTGCAGTTCCTAGTTTAAAG
 TAGAGCTTTACCTGTGATGTCATCAGCAAGAAATCATAGGCACTTTTAAATAAAGGTTTTAAAGTTTTTGGAAATCTCA
 GTGTATTTGCATCATAGAAAATGTCTGACTGTTTGCAAAATAATATTCTGTTTTAAGAATCCATCTTACCTCTCTTT
 AAGTTTCCATACACTTGAGAGCCAAACAACATATTTATTACTAAAAAGATGCTTTGCTAGAACTCAAAAACAGCA
 CTTCTTTTGGCACTTCTGCCCAGTTTTCTCTTTGCTTTAAATGAACATCATCATATGGAATTGGAATAGGAGAGTA
 TGAGTACGGCAGAGAAGTGGATCAGAAAACTAGAATGAGGATAAACATTTACATTAGTGGAACTCCTGAAATAAA
 TCCTTGATATTGTGAGTAACTGATTTTCAACAAGGATGCCAAGACAAAAGGCTTTTCAACAAACCGTGTGTTTTA
 AGAACAGACCTAAGTGGTTTAAATCACCCACTTTAGATGGGTGAATGTTATGGTGTGTGAAATATCTCAGTAAAGCA
 GTTAAAGGAAAAAGAGCTGGAATGCACTGATTGAGGAACCTTAATTTAGGAAGGAAAGGTCTGTATGTACACATTT
 CACTTTAAGCAGAAAAATCTTTCTCAAGAAATGACTTTACTTTCTTTGCACTGCCAGCACGTGAGATACTAACTT
 TTTAACTAGTTGTTCTCTCTAGTCTCTACGTTATTAGNATTTTTTGCTTTCATAATGTGAAACCTTTAAGCAGGAG
 AAGAAAAATGTTTTAGATAGTTTCAAATACNCCAAAAATGTTTGAACACAAAAATACTGGAATCNAACCATAATGC
 CCTTATTGAATATATAGTTGTATAGNTTGTCTGAAAACCC

>Final LGR7-S ORF (722 amino acids) (SEQ ID NO:08)

MTSGSVFFYILIFGKYFSGGGQDVKCSLGYFP CGNITKCLPQLLHCNGVDDCGNQADEDNVVLQCMSLPGLEL
 DWMKPFSTVPSVSSNVTAMSLQWNLRKLPDCFKNYHDLQKLDLQNNKITSISIYAFRGLNSLTKLYLSHNRITFL
 KPGVFEDLHRLEWLIIEDNHLRSISPPTFYGLNSLILLVLMNNVLRPLDPKPLCQHMPRLHWDLEGNHIIHNLRLNT
 FISCSNLTVLVMRKNKINHLNENTFAPLQKLELDLGSNKIENLPPLIFKDLKELSQLNLSYNPIQKIQANQFDYLV
 KLKLSLEGIEISNIQRMFRPLMNLSHIYFKKFQYCGYAPHVRSCKPNTDGISSLENLLASIIQRVFWVVSVAVTC
 FGNIFVICMRPYIRSENKLYAMSIISLCCADCLMGIYLFVIGGFDLKRGEYNKHAQLWMESTHCQLVGSLLAILSTE
 VSVLLLTFLTLKEYICIVYFRCVVRPGKCRITITVLILIIWITGFIYAFIPLSNKEFFKNYGYTNGVCFPLHSEDTESI
 GAQIYSVAIFLGINLAAFIIVFSYGSMSFYSVHQSATATEIRNQVKEMILAKRFFFIVFTDALCWIPIFVVKFLS
 LLQVEIPGTITSWVFIPLPINSALNPILYTLTRPFKEMIHRFWYNYRQRKSMSDSKGQKTYAPSFIVWEMWPLQEM
 PPELMPDLFTYPCEMSLISQSTRLNSYS*

FIG. 4

5/8

>Alignment of LGR7-L with LGR7-S

Query=LGR7-L

Sbjct=LGR7-S

```

Query: 1  MTSGSVFFYILIFGKYFSHGGGQDVKCSLGYFPCGNITKCLPQLLHCNGVDDCGNQADED 60
Sbjct: 1  MTSGSVFFYILIFGKYFSHGGGQDVKCSLGYFPCGNITKCLPQLLHCNGVDDCGNQADED 60

Query: 61  NCGDNNGWSMQFDKYFASYKMTSQYPFEAETPECLVGSVPVQCLCQ---GLELDCDETN 117
          NC                               V V C C      GLELD  +
Sbjct: 61  NC-----VVVLCQCMSLPGLELDWMKP- 82

Query: 118 LRAVPSVSSNVTAMSLQWNLIRKLPPDCFKNYHDLQKLYLQNNKITSISIIYAFRGLNSLT 177
          +VPSVSSNVTAMSLQWNLIRKLPPDCFKNYHDLQKL  LQNNKITSISIIYAFRGLNSLT
Sbjct: 83  FTSVPSVSSNVTAMSLQWNLIRKLPPDCFKNYHDLQKLDLQNNKITSISIIYAFRGLNSLT 142

Query: 178 KLYLSHNRITFLKPGVFEDLHRLEWLIIEDNHLRSRISPTFYGLNSLILLVLMNNVLTSL 237
          KLYLSHNRITFLKPGVFEDLHRLEWLIIEDNHLRSRISPTFYGLNSLILLVLMNNVLTSL
Sbjct: 143 KLYLSHNRITFLKPGVFEDLHRLEWLIIEDNHLRSRISPTFYGLNSLILLVLMNNVLTSL 202

Query: 238 PDKPLCQHMPRLHWLDLEGNHIIHNLRLNLTFISCSNLTVLVMRKNKINHLNENTFAPLQKL 297
          PDKPLCQHMPRLHWLDLEGNHIIHNLRLNLTFISCSNLTVLVMRKNKINHLNENTFAPLQKL
Sbjct: 203 PDKPLCQHMPRLHWLDLEGNHIIHNLRLNLTFISCSNLTVLVMRKNKINHLNENTFAPLQKL 262

Query: 298 DELDLGSNKIENLPPLIFKDLKELSQLNLSYNPIQKIQANQFDYLVKLKSLSLLEGIEISN 357
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Sbjct: 263 DELDLGSNKIENLPPLIFKDLKELSQLNLSYNPIQKIQANQFDYLVKLKSLSLLEGIEISN 322

Query: 358 IQQRMFRPLMNLSHIYFKKFQYCGYAPHVRSCKPNTDGISSLENLLASIIQRFVFWVWSA 417
          IQQRMFRPLMNLSHIYFKKFQYCGYAPHVRSCKPNTDGISSLENLLASIIQRFVFWVWSA
Sbjct: 323 IQQRMFRPLMNLSHIYFKKFQYCGYAPHVRSCKPNTDGISSLENLLASIIQRFVFWVWSA 382

Query: 418 VTCFGNIFVICMRPYIRSENKLYAMSIISLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQ 477
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Sbjct: 383 VTCFGNIFVICMRPYIRSENKLYAMSIISLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQ 442

Query: 478 LWMESTHCQLVGSAILSTEVSLLLLTFLTLEKYICIVYPPRCVPRPGKCRITITVLILIWI 537
          LWMESTHCQLVGSAILSTEVSLLLLTFLTLEKYICIVYPPRCVPRPGKCRITITVLILIWI
Sbjct: 443 LWMESTHCQLVGSAILSTEVSLLLLTFLTLEKYICIVYPPRCVPRPGKCRITITVLILIWI 502

Query: 538 TGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINLAAFIIIVF 597
          TGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINLAAFIIIVF
Sbjct: 503 TGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINLAAFIIIVF 562

Query: 598 SYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPFVVKFLSLLQVEI 657
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Sbjct: 563 SYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDALCWIPFVVKFLSLLQVEI 622

Query: 658 PGTITSWVVFILPINSALNPILYTLTTRPFKEMIHRFWYNRQRKSMDSGQKTYAPSF 717
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Sbjct: 623 PGTITSWVVFILPINSALNPILYTLTTRPFKEMIHRFWYNRQRKSMDSGQKTYAPSF 682

Query: 718 IWVEMWPLQEMPELMPDLFTYPCMSLISQSTRLNSYS 757
          IWVEMWPLQEMPELMPDLFTYPCMSLISQSTRLNSYS
Sbjct: 683 IWVEMWPLQEMPELMPDLFTYPCMSLISQSTRLNSYS 722

```

FIG. 5

6/8

FIG. 6

LGR4 MPPGLGLLCLFALGLLGSAGPSGA
LGR5 MDT SRLGVLLSLPVLQLLATG
LHR MKQRFSAQLLKL LLLQLPPLPRA
FSHR MALLLVSLLAFLSLGSG
TSHR MRPADLLQLVLLLDLPRDLGG

LGR4	APPL	AA-P	S	DGDR---	RVD	SGKGLTAVPEGLSAFTQA
LGR5	GSSPRSGVLLRG	P-TH	H	EPDGRMLLRVD		SDLGLSELPSNLSVFTSY
LHR	LREAL	P-EP	N	VPDG--ALR--		PGPTAGLTR
FSHR		HHRI	H	SNRVFL----		QSKVTEIPSDLPNAIE
TSHR	MG	SSPP	E	HOEED--FRVT		KDIORIPSLPPSTOT

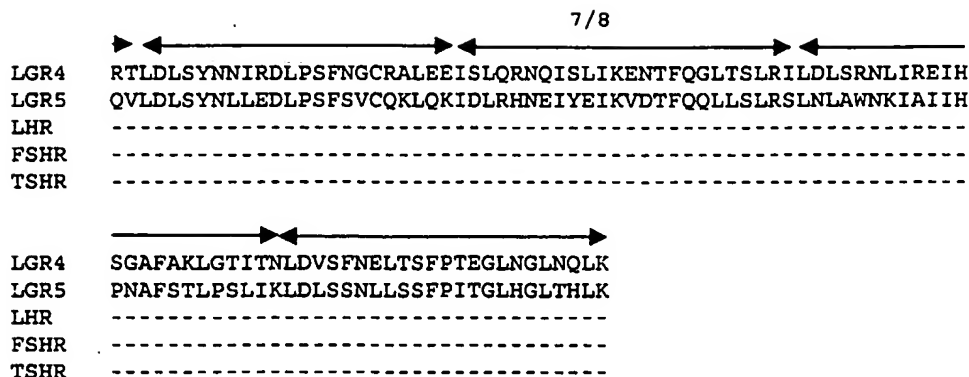
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LGR4	RTV	SE	IHG	SA	QS	RLDA	H-	TSV	EDS--	FEGLVQLRH	WLD	S-L-	EV	VR
LGR5	RHV-	TE	LQN	RS	QS	RLDA	H-	SYV	P-SC-	FSGLHSLRH	WLD	A-L-	E	VQ
LHR	RYIE	-G	FIN	PN	KY	SIC-	TG	RKF	DVTKVFSSES	NFI-	EIC	LHI-	T	GN
FSHR	LYIN	-E	FQN	PG	QY	LIS-	TG	KHL	DVHK-	IHSLQKVL-	DIQ	INI-	H-	ERN
TSHR	TYID	-D	LKE	PL	KF	GIF-	TGLKMF	DLTK-	VYSTDI	FFI	EIT	PYM-	S	VN

LGR4	PLSN	P-TLQA	T	AL	NISSIPDF	T	LSS	VV	H	HN	K-IKSLSQHC	D	LDN-LE	
LGR5	A	RS	S-ALQAMT	AL	KIHHPDY	G	LSSWVV	H	HN	R-IHSLGKKC	D	LHS-LE		
LHR	A	QGMNNE	SVT	K	YG	GFEEVQSH	-	GTT	TS	E	KE	VHLEKMHNGA	R	A-TGPK
FSHR	S	VG	SFESVI	W	NK	GIEQIHNC	-	GTQ	DE	N	SD	NNLEELPNDV	H	A-SGPV
TSHR	A	QG	CNETLT	K	YN	GFTSVQGY	-	GTK	DAVY	NK	KYLTVIDKDA	G	VXSGPV	

LGR4	T	LNYNYLDEF	Q-AIKA PS	KELGFHSNSISVI	D-GA GGNPL	RTIH -	DNPLS
LGR5	T	LNYNLDEF	T-AIRT SN	KELGFHSNNIRSI	E-KA VGNPS	ITIHF-	DNPIQ
LHR	T	ISSTKLQAL	SYGLESIQR	I-ATS-SYSLKKL	SRET V-N--	LEAT T	----
FSHR	I	ISRTRIHSI	SYGLEN KK	R-ARSTYN-LKKL	TLEKLVA---	MEAS T	----
TSHR	L	VSQTSVTAL	SKGLEH KE	I-ARNTWT-LKKL	LSLS LH---	TRAD S	----

LGR4 FVGN⁺SAFHNLSDLHCLVIRGASLVQWFPNLTGTVHLES⁺LTGTGKISSIPDDLQCNQKML
LGR5 FVGRSAFQHLPELRTLT⁺LN⁺GA⁺SQITEFPDLTG⁺TANLES⁺LTGAISSLPQTVCNQLPNL
LHR -----
FSHR -----
TSHR -----

**C-flank cysteine-rich sequence**

LGR4	LVGNFKLKDALAARDFANLRSLSV YAYQ	WGCDLCKLNTEDNSPQEHSVTKEKGA
LGR5	LTGNHALQSLISSENFPELKVIEM YAYQ	GVCENAYKISNQWNKGDNSMDDLHKK
LHR	----- --SH	RNLPTKEQNFSSHISENFSKQCESTVR
FSHR	----- --SH	ANWRRQISELHPICNKSILRQEVDMT
TSHR	----- --SH	KNQKKIRGILESLMCNESSMQSLRQRK

LGR4	TDAANVTSTAENE HS-----
LGR5	DAGMFQAQDERDL DF-----
LHR	KVSNKTLYSSMLA SE-----
FSHR	QTRGQRSSLAEDN SS-----
TSHR	SVNALNSPLHQEY ENLGDSIVGYKEKSKFQDTHNNAHYVVFEEQEDEIIGFGQELKNP

LGR4	-----QIIIH T STGA K	YLLGSWMI
LGR5	-----LLDFEEDLKALHSVQ S SPGP K	HLLDGWLI
LHR	-----LSGWDYBYGFCLPKTPR- A EPDA N	DIMGYDFL
FSHR	YSRGFDMTYTEFDYDLCNEVDVT S KPDA N	DIMGYNIL
TSHR	QEETLQAFDSHYDYTCGDSSEDMV T KSDE N	DIMGYKFL

Transmembrane

	TM 1										TM 2														
LGR4	LTV	F	FLV	LLF	LL	ILTVFA	CSS	PASKL	FIGLIS	SVSNLLM	IYTGILTFL	AVSW													
LGR5	IGV	T	AV	LTC	AL	TSTVFR	PLYISPIKL	IGVIAAVNMLT	VSSAVL	G	AF	F													
LHR	VLI	L	NI	IMG	MT	LFVLLT	RYK	TVPRF	MCNLSFADFCM	LYLLLI	S	SQ	K												
FSHR	VLI	F	SI	ITG	II	LVILTT	QYK	TVPRF	MCNLAFADLCI	IYLLLI	S	IH	K												
TSHR	IVV	FVSL	LLG	VF	LLILLT	HYK	NVPRF	MCNLAFADFCM	MYLLLI	S	LY	H													

	TM 3												
LGR4	GRFAEFG	W	E	S	KV	SLA	S	SA	FL	LA	AV	SVFAKDLMKHGKSSH	QF
LGR5	GSFARHGAW	EN	V	HVI	LSI	S	FL	LAA	GFSVKYSAKFET	APFSSL			
LHR	GQYYNHA	D	Q	S	ST	FT	L	YT	VIT	WHTITYAIHLDDQ	LR	HA	
FSHR	SQYHNYA	D	Q	A	DA	FT	L	YT	AIT	WHTITHAMQLDC	VQ	HA	
TSHR	SEYYNHA	D	Q	P	NT	FT	L	YT	VIT	WYAITFAMRLDR	IR	HA	

FIG. 6 (CONT)

8/8

	TM 4				TM 5			
LGR4	QVAALLALLGAAVAGCF	FHGGQ	SASPL	FPTGETPSLGFTVTLVL	SL	LLMA		
LGR5	KVIILLCALLALTM AV	L G K	GASPL	LPFGEPSTMG MVALIL	SLC	LMMT		
LHR	ILIMLGGWLFSSLI ML	V V N	MKVS I F	MDVETTL SQV	ILTI LI	VV	FIIC	
FSHR	ASVMVMGWIFAF AA	LF IF I S	MKVS I	MDIDSPLSQL	VMSLLV	VL	VVIC	
TSHR	CAIMVGGWVCCFLL LL	V I S	AKVS I	MDTETPLALA	IVFVLT	IV	VIVC	

	TM 6			
LGR4	II T L	CNL-EKEDLSENSQSSVI	HV W	NCIFFC VA FSFAPLIT AIS SPEI
LGR5	IA T L	CNL-DKGDLENIW CSMV	HI L L	NCILNC VA LSF SLINLTF SPEV
LHR	AC I I	FAVRNPELMATNK	TKIA KM I	DFTCMA IS FAI AAFKVPL TVTN
FSHR	GC IHI	LTVRNPNI VSSSS	TRIA RM M	DFLCMA IS FAI ASLKVPL TVSK
TSHR	CCHV I	ITVRNPQYNPGDK	TKIA RM V	DFICMA IS YAL AILNKPL TVSN

	TM 7			
LGR4	M SVTLI	F LPA L	V VF N	
LGR5	I FI LVVV	LPA L	L IL N	
LHR	S VL VL	Y INS A	F AI T	
FSHR	A IL VL	H INS A	F AI T	
TSHR	S IL VL	Y LNS A	F AI T	

C-terminal tail

LGR4	PK KE WKL KRRVTRKHGSVSVS	ISSQGGCGEQDFYYDCGMYSHLQGNLTVCDCCESFL
LGR5	PH KE LVS RKQTYVWTRSKHPSLMS	INSDDVEKQSCDSTQALVTFTSSSITYDLPPSS
LHR	KT QR FFL LSKFGCCKRRRAELYRRKDFS	AYTSNCKNGFTGSNKPSQSTLKLSTLHCQG
FSHR	KN RR FFI LSKCGCYEMQAQIYRTETSS	TVHNTHPRNGHCSSAPRV TNGSTYILVPLS
TSHR	KA QR VFI LSKFGICKRQAQAYRGQRP	PKNSTDIQVQKVTHDMRQGLHNMEDVYELI

LGR4	LTKPVSCKHLIKSHS	CPVLTAASCQRPEAYWSDCGTQSAHSDYADEEDSFVSDSSDQVQA
LGR5	VPSPAYPVTESCHLSS	VAFVPCL
LHR	TALLDKTRYTEC	
FSHR	HLAQN	
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LGR4	CGRACFYQSRGFPLVRYAYNLQRVRD
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FIG. 6 (CONT)

SEQUENCE LISTING

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 Hsu, Yu Sheau
 Liang, Shan-Guang
 van der Spek, Petrus Johannes

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35      40      45
Thr Ala Val Pro Glu Gly Leu Ser Ala Phe Thr Gln Ala Leu Asp Ile
50      55      60
Ser Met Asn Asn Ile Thr Gln Leu Pro Glu Asp Ala Phe Lys Ser Phe
65      70      75      80
Pro Phe Leu Glu Glu Leu Gln Leu Ala Gly Asn Asp Leu Ser Leu Ile
85      90      95
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His Asn Asn Lys Ile Lys Ser Leu Ser Gln His Cys Phe Asp Gly Leu
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Ser Asn Ser Ile Ser Val Ile Pro Asp Gly Ala Phe Gly Gly Asn Pro
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Leu Leu Arg Thr Ile His Leu Tyr Asp Asn Pro Leu Ser Phe Val Gly
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Leu	Asn	Gly	Leu	Asn	Gln	Leu	Lys	Leu	Val	Gly	Asn	Phe	Lys	Leu	Lys	435	440	445	450
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 865 870 875 880
 Cys Pro Val Leu Thr Ala Ala Ser Cys Gln Arg Pro Glu Ala Tyr Trp
 885 890 895
 Ser Asp Cys Gly Thr Gln Ser Ala His Ser Asp Tyr Ala Asp Glu Glu
 900 905 910
 Asp Ser Phe Val Ser Asp Ser Ser Asp Gln Val Gln Ala Cys Gly Arg
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 Ala Cys Phe Tyr Gln Ser Arg Gly Phe Pro Leu Val Arg Tyr Ala Tyr
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 Asn Leu Gln Arg Val Arg Asp
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<212> PRT
<213> human

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Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu Ser Asn Leu Lys Glu Leu
 35          40          45
Gly Phe His Ser Asn Asn Ile Arg Ser Ile Pro Glu Lys Ala Phe Val
 50          55          60
Gly Asn Pro Ser Leu Ile Thr Ile His Phe Tyr Asp Asn Pro Ile Gln
 65          70          75          80
Phe Val Gly Arg Ser Ala Phe Gln His Leu Pro Glu Leu Arg Thr Leu
 85          90          95
Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu Phe Pro Asp Leu Thr Gly
100          105          110
Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr Gly Ala Gln Ile Ser Ser
115          120          125
Leu Pro Gln Thr Val Cys Asn Gln Leu Pro Asn Leu Gln Val Leu Asp
130          135          140
Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro Ser Phe Ser Val Cys Gln
145          150          155          160
Lys Leu Gln Lys Ile Asp Leu Arg His Asn Glu Ile Tyr Glu Ile Lys
165          170          175
Val Asp Thr Phe Gln Gln Leu Leu Ser Leu Arg Ser Leu Asn Leu Ala
180          185          190
Trp Asn Lys Ile Ala Ile Ile His Pro Asn Ala Phe Ser Thr Leu Pro
195          200          205
Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn Leu Leu Ser Ser Phe Pro
210          215          220
Ile Thr Gly Leu His Gly Leu Thr His Leu Lys Leu Thr Gly Asn His
225          230          235          240
Ala Leu Gln Ser Trp Ile Ser Ser Glu Asn Phe Pro Glu Leu Lys Val
245          250          255
Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys Ala Phe Gly Val Cys Glu
260          265          270
Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn Lys Gly Asp Asn Ser Ser
275          280          285
Met Asp Asp Leu His Lys Lys Asp Ala Gly Met Phe Gln Ala Gln Asp
290          295          300
Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp Phe Glu Glu Asp Leu Lys
305          310          315          320
Ala Leu His Ser Val Gln Cys Ser Pro Ser Pro Gly Pro Phe Lys Pro
325          330          335
Cys Glu His Leu Leu Asp Gly Trp Leu Ile Arg Ile Gly Val Trp Thr
340          345          350

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Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile Lys Leu Leu Ile Gly Val
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Ile Ala Ala Val Asn Met Leu Thr Gly Val Ser Ser Ala Val Leu Ala
385                      390                      395                      400
Gly Val Asp Ala Phe Thr Phe Gly Ser Phe Ala Arg His Gly Ala Trp
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Trp Glu Asn Gly Val Gly Cys His Val Ile Gly Phe Leu Ser Ile Phe
    420                      425                      430
Ala Ser Glu Ser Ser Val Phe Leu Leu Thr Leu Ala Ala Leu Glu Arg
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Gly Phe Ser Val Lys Tyr Ser Ala Lys Phe Glu Thr Lys Ala Pro Phe
    450                      455                      460
Ser Ser Leu Lys Val Ile Ile Leu Leu Cys Ala Leu Leu Ala Leu Thr
465                      470                      475                      480
Met Ala Ala Val Pro Leu Leu Gly Gly Ser Lys Tyr Gly Ala Ser Pro
    485                      490                      495
Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro Ser Thr Met Gly Tyr Met
    500                      505                      510
Val Ala Leu Ile Leu Leu Asn Ser Leu Cys Phe Leu Met Met Thr Ile
    515                      520                      525
Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp Lys Gly Asp Leu Glu Asn
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Ile Trp Asp Cys Ser Met Val Lys His Ile Ala Leu Leu Leu Phe Thr
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Val Val Val Pro Leu Pro Ala Cys Leu Asn Pro Leu Leu Tyr Ile Leu
    595                      600                      605
Phe Asn Pro His Phe Lys Glu Asp Leu Val Ser Leu Arg Lys Gln Thr
    610                      615                      620
Tyr Val Trp Thr Arg Ser Lys His Pro Ser Leu Met Ser Ile Asn Ser
625                      630                      635                      640
Asp Asp Val Glu Lys Gln Ser Cys Asp Ser Thr Gln Ala Leu Val Thr
    645                      650                      655
Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu Pro Pro Ser Ser Val Pro
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Phe Val Pro Cys Leu
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<211> 2467
<212> DNA
<213> human

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<211> 757
<212> PRT
<213> human

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Pro Cys Gly Asn Ile Thr Lys Cys Leu Pro Gln Leu Leu His Cys Asn
35          40          45
Gly Val Asp Asp Cys Gly Asn Gln Ala Asp Glu Asp Asn Cys Gly Asp
50          55          60
Asn Asn Gly Trp Ser Met Gln Phe Asp Lys Tyr Phe Ala Ser Tyr Tyr
65          70          75          80
Lys Met Thr Ser Gln Tyr Pro Phe Glu Ala Glu Thr Pro Glu Cys Leu
85          90          95
Val Gly Ser Val Pro Val Gln Cys Leu Cys Gln Gly Leu Glu Leu Asp
100         105         110
Cys Asp Glu Thr Asn Leu Arg Ala Val Pro Ser Val Ser Ser Asn Val
115         120         125
Thr Ala Met Ser Leu Gln Trp Asn Leu Ile Arg Lys Leu Pro Pro Asp
130         135         140

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Cys	Phe	Lys	Asn	Tyr	His	Asp	Leu	Gln	Lys	Leu	Tyr	Leu	Gln	Asn	Asn	145	150	155	160
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Thr	Lys	Leu	Tyr	Leu	Ser	His	Asn	Arg	Ile	Thr	Phe	Leu	Lys	Pro	Gly	180	185	190	
Val	Phe	Glu	Asp	Leu	His	Arg	Leu	Glu	Trp	Leu	Ile	Ile	Glu	Asp	Asn	195	200	205	
His	Leu	Ser	Arg	Ile	Ser	Pro	Pro	Thr	Phe	Tyr	Gly	Leu	Asn	Ser	Leu	210	215	220	
Ile	Leu	Leu	Val	Leu	Met	Asn	Asn	Val	Leu	Thr	Arg	Leu	Pro	Asp	Lys	225	230	235	240
Pro	Leu	Cys	Gln	His	Met	Pro	Arg	Leu	His	Trp	Leu	Asp	Leu	Glu	Gly	245	250	255	
Asn	His	Ile	His	Asn	Leu	Arg	Asn	Leu	Thr	Phe	Ile	Ser	Cys	Ser	Asn	260	265	270	
Leu	Thr	Val	Leu	Val	Met	Arg	Lys	Asn	Lys	Ile	Asn	His	Leu	Asn	Glu	275	280	285	
Asn	Thr	Phe	Ala	Pro	Leu	Gln	Lys	Leu	Asp	Glu	Leu	Asp	Leu	Gly	Ser	290	295	300	
Asn	Lys	Ile	Glu	Asn	Leu	Pro	Pro	Leu	Ile	Phe	Lys	Asp	Leu	Lys	Glu	305	310	315	320
Leu	Ser	Gln	Leu	Asn	Leu	Ser	Tyr	Asn	Pro	Ile	Gln	Lys	Ile	Gln	Ala	325	330	335	
Asn	Gln	Phe	Asp	Tyr	Leu	Val	Lys	Leu	Lys	Ser	Leu	Ser	Leu	Glu	Gly	340	345	350	
Ile	Glu	Ile	Ser	Asn	Ile	Gln	Gln	Arg	Met	Phe	Arg	Pro	Leu	Met	Asn	355	360	365	
Leu	Ser	His	Ile	Tyr	Phe	Lys	Lys	Phe	Gln	Tyr	Cys	Gly	Tyr	Ala	Pro	370	375	380	
His	Val	Arg	Ser	Cys	Lys	Pro	Asn	Thr	Asp	Gly	Ile	Ser	Ser	Leu	Glu	385	390	395	400
Asn	Leu	Leu	Ala	Ser	Ile	Ile	Gln	Arg	Val	Phe	Val	Trp	Val	Val	Ser	405	410	415	
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Cys	Ala	Asp	Cys	Leu	Met	Gly	Ile	Tyr	Leu	Phe	Val	Ile	Gly	Gly	Phe	450	455	460	
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Glu	Ser	Thr	His	Cys	Gln	Leu	Val	Gly	Ser	Leu	Ala	Ile	Leu	Ser	Thr	485	490	495	
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Cys	Ile	Val	Tyr	Pro	Phe	Arg	Cys	Val	Arg	Pro	Gly	Lys	Cys	Arg	Thr	515	520	525	
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Ile	Pro	Leu	Ser	Asn	Lys	Glu	Phe	Phe	Lys	Asn	Tyr	Tyr	Gly	Thr	Asn	545	550	555	560
Gly	Val	Cys	Phe	Pro	Leu	His	Ser	Glu	Asp	Thr	Glu	Ser	Ile	Gly	Ala	565	570	575	
Gln	Ile	Tyr	Ser	Val	Ala	Ile	Phe	Leu	Gly	Ile	Asn	Leu	Ala	Ala	Phe	580	585	590	
Ile	Ile	Ile	Val	Phe	Ser	Tyr	Gly	Ser	Met	Phe	Tyr	Ser	Val	His	Gln	595	600	605	

Ser Ala Ile Thr Ala Thr Glu Ile Arg Asn Gln Val Lys Lys Glu Met
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Pro Cys Gly Asn Ile Thr Lys Cys Leu Pro Gln Leu Leu His Cys Asn
35          40          45
Gly Val Asp Asp Cys Gly Asn Gln Ala Asp Glu Asp Asn Cys Val Val
50          55          60
Val Leu Cys Gln Cys Met Ser Leu Pro Gly Leu Glu Leu Asp Trp Met
65          70          75          80
Lys Pro Phe Thr Ser Val Pro Ser Val Ser Asn Val Thr Ala Met
85          90          95
Ser Leu Gln Trp Asn Leu Ile Arg Lys Leu Pro Pro Asp Cys Phe Lys
100         105         110
Asn Tyr His Asp Leu Gln Lys Leu Asp Leu Gln Asn Asn Lys Ile Thr
115         120         125
Ser Ile Ser Ile Tyr Ala Phe Arg Gly Leu Asn Ser Leu Thr Lys Leu
130         135         140
Tyr Leu Ser His Asn Arg Ile Thr Phe Leu Lys Pro Gly Val Phe Glu
145         150         155         160
Asp Leu His Arg Leu Glu Trp Leu Ile Ile Glu Asp Asn His Leu Ser
165         170         175
Arg Ile Ser Pro Thr Phe Tyr Gly Leu Asn Ser Leu Ile Leu Leu
180         185         190

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His Asn Leu Arg Asn Leu Thr Phe Ile Ser Cys Ser Asn Leu Thr Val
    225                230                235                240
Leu Val Met Arg Lys Asn Lys Ile Asn His Leu Asn Glu Asn Thr Phe
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Ala Pro Leu Gln Lys Leu Asp Glu Leu Asp Leu Gly Ser Asn Lys Ile
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Glu Asn Leu Pro Pro Leu Ile Phe Lys Asp Leu Lys Glu Leu Ser Gln
    275                280                285
Leu Asn Leu Ser Tyr Asn Pro Ile Gln Lys Ile Gln Ala Asn Gln Phe
    290                295                300
Asp Tyr Leu Val Lys Leu Lys Ser Leu Ser Leu Glu Gly Ile Glu Ile
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Ser Asn Ile Gln Gln Arg Met Phe Arg Pro Leu Met Asn Leu Ser His
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Ile Tyr Phe Lys Lys Phe Gln Tyr Cys Gly Tyr Ala Pro His Val Arg
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Cys Phe Gly Asn Ile Phe Val Ile Cys Met Arg Pro Tyr Ile Arg Ser
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Cys Leu Met Gly Ile Tyr Leu Phe Val Ile Gly Gly Phe Asp Leu Lys
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His Cys Gln Leu Val Gly Ser Leu Ala Ile Leu Ser Thr Glu Val Ser
    450                455                460
Val Leu Leu Leu Thr Phe Leu Thr Leu Glu Lys Tyr Ile Cys Ile Val
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    485                490                495
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    515                520                525
Phe Pro Leu His Ser Glu Asp Thr Glu Ser Ile Gly Ala Gln Ile Tyr
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Ser Val Ala Ile Phe Leu Gly Ile Asn Leu Ala Ala Phe Ile Ile Ile
    545                550                555                560
Val Phe Ser Tyr Gly Ser Met Phe Tyr Ser Val His Gln Ser Ala Ile
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Lys Arg Phe Phe Phe Ile Val Phe Thr Asp Ala Leu Cys Trp Ile Pro
    595                600                605
Ile Phe Val Val Lys Phe Leu Ser Leu Leu Gln Val Glu Ile Pro Gly
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    625                630                635                640
Leu Asn Pro Ile Leu Tyr Thr Leu Thr Thr Arg Pro Phe Lys Glu Met
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Ile	His	Arg	Phe	Trp	Tyr	Asn	Tyr	Arg	Gln	Arg	Lys	Ser	Met	Asp	Ser
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		675					680					685			
Pro	Leu	Gln	Glu	Met	Pro	Pro	Glu	Leu	Met	Lys	Pro	Asp	Leu	Phe	Thr
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Tyr	Pro	Cys	Glu	Met	Ser	Leu	Ile	Ser	Gln	Ser	Thr	Arg	Leu	Asn	Ser
705					710					715					720
Tyr	Ser														

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/06573

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C07K 14/705; C12N 15/12, 15/63, 15/70, 15/79

US CL :530/350; 435/69.1, 252.3, 254.11, 320.1, 325

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/350; 435/69.1, 252.3, 254.11, 320.1, 325

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, Biosis, Medline, WPI

search terms: G-protein coupled receptor, Leucine rich repeats, Gonadotropin receptor, Thyrotropin receptor

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 5,614,363 A (CONE) 25 March 1997, entire document.	1-11
X, P ----- Y, P	US 5,858,716 A (ELSHOURBAGY et al.) 12 January 1999, columns 20-30, entire document.	11 ----- 1-10
X -- Y	HWANG et al. Analysis of Expressed Sequence Tags from a Fetal Human Heart cDNA Library. Genomics. 1995, Vol. 30, pages 293-298, entire document.	5, 7, 11 ----- 1-4, 6, 8-10

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
B earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

11 JUNE 1999

Date of mailing of the international search report

02 AUG 1999

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/06573

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claims 1-11, drawn to nucleic acids encoding LGR4, the LGR4 polypeptide, and method of using the LGR4 nucleic acid.

Group II, claims 1-11, drawn to nucleic acids encoding LGR5, the LGR5 polypeptide and method of using the LGR5 nucleic acid.

Group III, claims 1-11, drawn to nucleic acid encoding LGR6, the LGR6 polypeptide, and method of using the LGR6 nucleic acid.

Group IV, claims 12 and 13, drawn to antibody that binds to LGR4.

Group V, claims 12 and 13, drawn to antibody that binds to LGR5.

Group VI, claims 12 and 13, drawn to antibody that binds to LGR7.

Group VII, claims 14-17, drawn to transgenic animal model containing an altered LGR4 gene.

Group VIII, claims 14-17, drawn to transgenic animal model containing an altered LGR5 gene

Group IX, claims 14-17, drawn to transgenic animal model containing an altered LGR7 gene

Group X, claim 18, drawn to a method of screening for a ligand for LGR4.

Group XI, claim 18, drawn to a method of screening for a ligand for LGR5.

Group XII, claim 18, drawn to a method of screening for a ligand for LGR7.

Each of the claims 1-18 is in three different groups because LGR4, LGR5, and LGR7 are structurally and functionally distinct polypeptides.

The inventions listed as Groups I-XII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The special technical feature of Group I is the nucleic acid sequence encoding LGR4. The special technical feature of Group II is the nucleic acid sequence encoding LGR5. The special technical feature of Group III is the nucleic acid sequence encoding LGR7. The special technical feature of Group IV is the antibody that binds to LGR4 but does not have the amino acid sequence of LGR4. The special technical feature of Group V is the antibody that binds to LGR5 but does not have the amino acid sequence of LGR5. The special technical feature of Group VI is the antibody that binds to LGR6 but does not have the amino acid sequence of LGR6. The special technical feature of Group VII is a transgenic animal containing an altered LGR4 gene. The special technical feature of Group VIII is a transgenic animal containing an altered LGR5 gene. The special technical feature of Group IX is a transgenic animal containing an altered LGR7 gene. The special technical feature of Group X is a method of screening for a ligand that binds LGR4. The special technical feature of Group XI is a method of screening for a ligand that binds LGR5. The special technical feature of Group XII is a method of screening for a ligand that binds LGR7. The special technical feature of each group is not the same or does not correspond to the special technical feature of any other group because the products of Groups I-IX are structurally and functionally distinct and the methods of Groups I-III and X-XII are distinct methods of using different starting reagent for accomplishing different goals. The groups are not linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept.

INTERNATIONAL SEARCH REPORT**International application No.**
PCT/US99/06573**C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P	HSU et al. Characterization of Two LGR Genes Homologous to Gonadotropin and Thyrotropin Receptors with Extracellular Leucine-Rich Repeats and a G Protein-Coupled, Seven Transmembrane Region. Molecular Endocrinology. December 1998, Vol. 12, No. 12, pages 1830-1845, especially pages 1831-1837.	1-11